

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Mismatch				
1	21	100.0	0	21	2	AAT37370	Bacteriophage T4
2	21	100.0	0	21	4	AAF61417	E. coli
3	21	100.0	0	21	6	ABF76597	Recombinant
4	21	100.0	0	21	7	ACC44645	Recombinant
5	21	100.0	0	25	2	AAC47894	Nucleotide
6	21	100.0	0	25	3	AAC55600	Oligonucleotide
7	21	100.0	0	25	4	AAC87897	Recombinant
8	21	100.0	0	25	4	AAC87896	PCR primer
9	21	100.0	0	25	4	AAF55765	Escherichia coli
10	21	100.0	0	25	4	AAF55766	Recombinant
11	21	100.0	0	25	4	AAD14459	PCR primer
12	21	100.0	0	25	8	ACD28426	Recombinant
13	21	100.0	0	25	8	ACD28427	Wild type
14	21	100.0	0	25	8	ACD28427	Engineered
15	21	100.0	0	25	8	ACD28605	Wild type
16	21	100.0	0	25	8	ACD28606	Engineered
17	21	100.0	0	25	8	ADA38193	Complemen
18	21	100.0	0	25	8	ADA38192	DNA of a
19	21	100.0	0	25	9	AAD60588	attBwt ol
20	21	100.0	0	27	4	AAS06174	Phage-lam
21	21	100.0	0	27	4	AAF61422	AttB DNA
22	21	100.0	0	27	7	ABZ58727	Att site
23	21	100.0	0	27	7	ACC59571	Nucleic acid

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Query Match      100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 2
AAF61417
ID AAF61417 standard; DNA; 21 BP.
XX AC AAF61417;
XX DT 05-JUN-2001 (first entry)
XX DE E. coli attB DNA fragment.
XX KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
XX OS targeted integration; attB; ds.
XX DN DEL9941186-A1.
XX PD 01-MAR-2001.
XX PF 30-AUG-1999; 99DE-01041186.
XX PR 30-AUG-1999; 99DE-01041186.
XX PA (DROE/) DROEGE P.
XX PI Droege P;
XX DR WPI; 2001-246016/26.
XX PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
XX for somatic cell gene therapy, uses an integrase to effect recombination
XX between att sites.
XX PS Claim 2; Page 13; 24pp; German.
XX CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (1) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC a vector containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences
XX
SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match      100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 3
ABS76597
ID ABS76597 standard; DNA; 21 BP.
XX AC ABS76597;
XX DT 05-JUN-2001 (first entry)
XX DE E. coli attB DNA fragment.
XX KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
XX OS targeted integration; attB; ds.
XX DN DEL9941186-A1.
XX PD 01-MAR-2001.
XX PF 30-AUG-1999; 99DE-01041186.
XX PR 30-AUG-1999; 99DE-01041186.
XX PA (DROE/) DROEGE P.
XX PI Droege P;
XX DR WPI; 2001-246016/26.
XX PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
XX for somatic cell gene therapy, uses an integrase to effect recombination
XX between att sites.
XX PS Claim 2; Page 13; 24pp; German.
XX CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (1) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC a vector containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences
XX
SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match      100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 4
ACC44645
ID ACC44645 standard; DNA; 21 BP.
XX AC ACC44645;
XX DT 29-MAY-2003 (first entry)
XX DE Nucleotide core region of attB SEQ ID NO:34.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
XX FN
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```
DT 11-DEC-2002 (first entry)
XX Recombinase recognition site attB.
DE
XX
XX Respondent cell; expression construct; screening assay; gene regulation;
KW biosensor; reporter gene construct; recombinase recognition site; ds.
XX
XX Synthetic.
XX
XX WO200272789-A2.
XX PN
XX 19-SEP-2002.
XX PD
XX 12-MAR-2002; 2002WO-US080008.
XX PF
XX 12-MAR-2001; 2001US-0274979P.
XX PR
XX 12-MAR-2001; 2001US-0275070P.
XX PR
XX 12-MAR-2001; 2001US-0275148P.
XX PR
XX (IRMI-) IRM LLC.
XX PA
XX Caldwell JS, Su AI, Hogenesch JB;
XX PI
XX WPI; 2002-723339/78.
XX DR
XX
XX Producing a collection of responder cells for high throughput screening
XX assays, comprises identifying and cloning regulatory regions into
XX expression constructs to control nucleic acids, and introducing into
XX addressable cells.
XX
XX Disclosure; Page 179; 187pp; English.
XX
XX The invention describes producing a collection of responder cells for
XX high throughput screening assays, by identifying and cloning regulatory
XX regions into expression constructs to control nucleic acids, and
XX introducing the constructs into addressable cells. The method is useful
XX in producing cells used in high throughput screening assays for profiling
XX substances and conditions and for studying the function of the regulatory
XX region mediating the response. The cells serve as biosensors to assess
XX the effects of any perturbation, such as external or internal condition,
XX on the cells from which the regulatory regions in the reporter gene
XX constructs are derived can be inferred. This sequence represents a
XX recombinase recognition site that can be incorporated into the expression
XX constructs of the invention
XX
XX Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 4
ACC44645
ID ACC44645 standard; DNA; 21 BP.
XX AC ACC44645;
XX DT 29-MAY-2003 (first entry)
XX DE Nucleotide core region of attB SEQ ID NO:34.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
XX FN
```

XX PD 05-DEC-2002.
 XX PF 30-MAY-2002; 2002WO-US017452.
 XX PR 30-MAY-2001; 2001US-0294758P.
 XX PR 21-MAR-2002; 2002US-0366891P.
 XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 XX PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 XX PI Stewart S, Shellard J;
 XX DR WPI; 2003-140461/13.
 XX PT Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest.
 XX PS Disclosure; Fig 6; 272pp; English.
 XX CC The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96857 represent sequences used in the
 CC exemplification of the present invention
 XX SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred.No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATACTACTTG 21
 Db 1 CTGCTTTTATACTACTTG 21
 RESULT 5
 AAX78994
 ID AAX78994 standard; DNA; 25 BP.
 XX AC AAX78994;
 XX DT 17-AUG-1999 (first entry)
 XX DE Oligonucleotide #60 for recombination and cloning method.
 XX KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX OS Synthetic.
 XX PN WO9921977-A1.
 XX PD 06-MAY-1999.
 XX PF 26-OCT-1998; 98WO-US022589.
 XX

PR 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX DR WPI; 1999-303011/25.
 XX PT New nucleic acid cloning methods.
 XX PS Disclosure; Page 176; 185pp; English.
 XX CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred.No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATACTACTTG 21
 Db 4 CTGCTTTTATACTACTTG 24
 RESULT 6
 AAC55600/c
 ID AAC55600 standard; DNA; 25 BP.
 XX AC AAC55600;
 XX DT 11-JAN-2001 (first entry)
 XX DE Recombination efficiency with mutated attB2 site oligonucleotide attB0.
 XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX KW mutant; recombinational cloning; entry vector; destination vector;
 XX KW gene product targeting; fusion tag cleavage; PCR primer; ss.
 XX OS Bacteriophage lambda.
 XX OS Synthetic.
 XX PN WO200052027-A1.
 XX PD 08-SEP-2000.
 XX PF 02-MAR-2000; 2000WO-US005432.
 XX PR 02-MAR-1999; 99US-0122389P.
 XX PR 23-MAR-1999; 99US-0126049P.
 XX PR 28-MAY-1999; 99US-0136744P.
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX PI Hartley JL, Brasch MA, Temple GF, Chao D;
 XX DR WPI; 2000-543948/49.
 XX

PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
XX Example 23; Page 157; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is used
XX in the exemplification of the present invention
XX
XX Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 22 CTGCTTTTATATACTAACTTG 2

RESULT 7
AAS06276/c
ID AAS06276 standard; DNA; 25 BP.

AC AAS06276;

XX 12-SEP-2001 (first entry)

XX PCR primer attB0 used to produce a population of hybrid DNA molecules.
XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.

XX Bacteriophage lambda.

XX Synthetic.

XX W0200142509-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033546.

XX 10-DEC-1999; 99US-0169983P.

XX 09-MAR-2000; 2000US-0188020P.

XX (CHEO/) CHEO D.

XX (BRAS/) BRASCH M A.

XX (TEMP/) TEMPLE G F.

XX (HART/) HARTLEY J L.

XX (BYRD/) BYRD D R N.

XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

DR WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
XX more recombination sites in the presence of recombination proteins, e.g.
XX Cre.
XX
XX Example 11; Page 227; 357pp; English.

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX nucleic acid sequences, and PCR primers of the invention. The att
XX sequences are recognised by the recombination protein lambda integrase
XX (Int). The invention is a new method of producing a population of hybrid
XX nucleic acids comprising mixing at least a first population of nucleic
XX acids comprising one or more recombination sites with at least one target
XX nucleic acid comprising one or more recombination sites and causing some
XX or all of the nucleic acids to recombine with all or some of the target
XX nucleic acids. The method is useful for producing a population of hybrid
XX nucleic acids which may be the same or different. The nucleic acids may
XX be used to express therapeutic proteins or peptides and they may also be
XX used to create novel fusion proteins by expressing different sequences
XX linked to each other. The method allows simultaneous cloning of two or
XX more different nucleic acids

SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 22 CTGCTTTTATATACTAACTTG 2

RESULT 8
AAC87897/c

ID AAC87897 standard; DNA; 25 BP.

XX AAC87897;

XX 02-MAR-2001 (first entry)

XX Escherichia coli attB oligonucleotide SEQ ID NO:32.

XX Core region; recombination site; cloning; chimeric DNA; PCR primer;
XX characteristic; mutation; att site; lox site; phoA gene; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.

XX Example 3; Col 24; 73pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acids; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive. The
CC present sequence represents an E. coli attB oligonucleotide, which is
CC used in an example from the present invention
XX
SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAACTTG 21
Db 22 CTGCTTTTATACTAACTTG 2

RESULT 9
ID AAC87896 standard; DNA; 25 BP.
XX AAC87896;
XX 02-WAR-2001 (first entry)
XX Escherichia coli attB oligonucleotide SEQ ID NO:31.
XX Core region; recombination site; cloning; chimeric DNA; PCR primer;
KW characteristic; mutation; att site; lox site; phoA gene; ss.
XX Escherichia coli.
XX US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX Example 3; Col 24; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first

CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acids; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive. The
CC present sequence represents an E. coli attB oligonucleotide, which is
CC used in an example from the present invention
XX
SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAACTTG 21
Db 4 CTGCTTTTATACTAACTTG 24

RESULT 10
AAF55765
ID AAF55765 standard; DNA; 25 BP.
XX AAF55765;
XX 12-APR-2001 (first entry)
XX Recombination site attBwt.
XX Recombination site; cloning; att; ss.
XX Unidentified.
XX US6171861-B1.
XX 09-JAN-2001.
XX 12-JAN-1998; 98US-00005476.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX Example 3; Col 23; 73pp; English.

XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention

RESULT 12
AAD14459
ID AAD1
XX

PN US2003064515-A1.
 XX
 PD
 XX 03-APR-2003.
 XX
 PF 30-JAN-2002; 2002US-00058291.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 XX (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 PI Hartley JL, Brasch MA;
 XX
 XX WPI; 2003-540791/51.
 DR
 XX
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Example 3; Page 13; 71pp; English.
 PS
 XX The invention relates to a vector donor DNA molecule comprising a first
 CC DNA segment and a second DNA segment containing at least one selectable
 CC marker. The first and second segments are separated either by, in a
 CC circular vector donor, a first and a second recombination site, or in a
 CC linear vector donor, at least a first recombination site, where each pair
 CC of flanking recombination sites are engineered and do not recombine with
 CC each other. The nucleic acid molecule, vectors and methods are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).
 CC The present sequence represents the wild type attL and attR site
 CC recombination sequence attB
 XX
 XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 21; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATTAACCTTG 21
 Db 4 CTGCTTTTATTAACCTTG 24
 RESULT 14
 ACD28427/c
 ID ACD28427 standard; DNA; 25 BP.
 XX
 AC ACD28427;
 XX
 XX 02-OCT-2003 (first entry)
 DT
 DE Engineered recombination site associated DNA #1.
 XX
 XX Vector donor DNA; ds; flanking recombination site.
 KW
 XX Synthetic.
 OS
 XX US2003064515-A1.
 PN
 XX 03-APR-2003.
 PD
 XX
 XX 30-JAN-2002; 2002US-00058291.
 PF
 XX
 XX 07-JUN-1995; 95US-00486139.
 PR
 XX 07-JUN-1996; 96US-00663002.
 PR
 XX 20-JAN-1999; 99US-00233493.
 PR
 XX 02-NOV-1999; 99US-00432085.

XX
 PA (HART/) HARTLEY J L.
 XX (BRAS/) BRASCH M A.
 XX
 PI Hartley JL, Brasch MA;
 XX
 XX WPI; 2003-540791/51.
 DR
 XX
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Disclosure; Page 24; 71pp; English.
 PS
 XX
 XX The invention relates to a vector donor DNA molecule comprising a first
 CC DNA segment and a second DNA segment containing at least one selectable
 CC marker. The first and second segments are separated either by, in a
 CC circular vector donor, a first and a second recombination site, or in a
 CC linear vector donor, at least a first recombination site, where each pair
 CC of flanking recombination sites are engineered and do not recombine with
 CC each other. The nucleic acid molecule, vectors and methods are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).
 CC The present sequence represents the engineered recombination site
 CC associated DNA #1
 XX
 XX Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 21; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATTAACCTTG 21
 Db 22 CTGCTTTTATTAACCTTG 2
 RESULT 15
 ACD28605
 ID ACD28605 standard; DNA; 25 BP.
 XX
 AC ACD28605;
 XX
 XX 09-OCT-2003 (first entry)
 DT
 XX
 DE Wild type attL and attR site recombination sequence attBwt.
 XX
 XX Cointegrate DNA; flanking recombination site; ds; attBwt.
 KW
 XX Synthetic.
 OS
 XX US2003068799-A1.
 PN
 XX 10-APR-2003.
 PD
 XX
 XX 06-JUN-2002; 2002US-00162879.
 PF
 XX
 XX 07-JUN-1995; 95US-00486139.
 PR
 XX 07-JUN-1996; 96US-00663002.
 PR
 XX 20-JAN-1999; 99US-00233493.
 PR
 XX 02-NOV-1999; 99US-00432085.
 XX
 XX (INVI-) INVITROGEN CORP.
 PA
 XX
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2003-540884/51.
 DR
 XX
 XX Making Cointegrate DNA molecule, by combining recombination sites
 PT flanking the desired DNA segment in insert donor DNA, with the
 PT recombination sites of vector donor DNA, using site specific

PT recombination protein.
 XX
 PS Example 3; Page 14; 71pp; English.
 XX
 CC The invention relates to a method of making a cointegrate DNA molecule.
 CC The method is useful for making a cointegrate DNA molecule. The method is
 CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
 CC vitro or in vivo. The method enables efficient and specific recombination
 CC of DNA segments using recombination proteins. The method is highly
 CC specific, rapid and less labour intensive. The improved specificity,
 CC yield and speed of the method facilitates DNA or RNA subcloning,
 CC regulation and exchange useful for other related purposes. Since single
 CC molecules of the recombinations product can be introduced into a
 CC biological host, propagation of the desired product DNA in the absence of
 CC other DNA molecules is more readily realised. Reaction conditions can be
 CC freely adjusted in vitro to optimise enzyme activities. The present
 CC sequence represents the wild type attL and attR site recombination
 CC sequence attBwt
 XX
 SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATTAATACTTG 21
 Db 4 CTGCTTTTATTAATACTTG 24

Search completed: September 9, 2004, 18:05:38
 Job time : 25.9144 secs

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Query Match      100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. NO. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  CTGCTTTTATTACTACTTG  21
        |||||
Db       1  CTGCTTTTATTACTACTTG  21
        |||||

RESULT 2
US-10-252-384-6
Sequence 6, Application US/10252384

```

Publication No. US2003010444A1
 GENERAL INFORMATION:
 APPLICANT: CROUZET, Joel
 SCHERMAN, Daniel
 CAMERON, Beatrice
 WILS, Pierre
 DARQUET, Anne-Marie
 TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND USE THEREOF IN GENE THERAPY
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, Mailstop 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/252,384
 FILING DATE: 24-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,511
 FILING DATE: <Unknown>
 APPLICATION NUMBER: FR 95/02117
 FILING DATE: 23-FEB-1995
 APPLICATION NUMBER: WO 96/00274
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Savitzky Esq., Martin F.
 REGISTRATION NUMBER: 29,699
 REFERENCE/DOCKET NUMBER: ST95013-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3816
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Oligonucleotide"
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-252-384-6

Query Match 100.0%; Score 21; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAACTTG 21
 DB 1 CTGCTTTTATCTAACTTG 21

RESULT 3
 US-10-161-403-34
 Sequence 34, Application US/10161403
 Publication No. US20030119104A1
 GENERAL INFORMATION:
 APPLICANT: Perkins, Edward
 APPLICANT: Perez, Carl
 APPLICANT: Lindenbaum, Michael
 APPLICANT: Greene, Amy
 APPLICANT: Leung, Josephine
 APPLICANT: Fleming, Elena
 APPLICANT: Stewart, Sandra
 APPLICANT: Shellard, Joan

TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
 FILE REFERENCE: 24601-420
 CURRENT APPLICATION NUMBER: US/10/161,403
 CURRENT FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: 60/294,758
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: 60/366,891
 PRIOR FILING DATE: 2002-03-21
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: attB
 US-10-161-403-34

Query Match 100.0%; Score 21; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAACTTG 21
 DB 1 CTGCTTTTATCTAACTTG 21

RESULT 4
 US-10-097-034A-45
 Sequence 45, Application US/10097034A
 Publication No. US20040076954A1
 GENERAL INFORMATION:
 APPLICANT: Su, Andrew
 APPLICANT: Hogenesch, John
 APPLICANT: Caldwell, Jeremy
 TITLE OF INVENTION: Genomics-driven High Speed Cellular Assays, Development Thereof
 TITLE OF INVENTION: Collections of Cellular Reporters
 FILE REFERENCE: 38417-1311
 CURRENT APPLICATION NUMBER: US/10/097,034A
 CURRENT FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: 60/275,148
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: 60/274,979
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: 60/275,070
 PRIOR FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 45
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: attB
 US-10-097-034A-45

Query Match 100.0%; Score 21; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAACTTG 21
 DB 1 CTGCTTTTATCTAACTTG 21

RESULT 5
 US-10-310-695-13
 Sequence 13, Application US/10310695
 Publication No. US20040110293A1
 GENERAL INFORMATION:
 APPLICANT: DROGE, PETER
 APPLICANT: ENENKEL, BARBARA
 TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS

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; FILE REFERENCE: DEBE:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: DNA
; LENGTH: 21
; ORGANISM: Escherichia coli
US-10-310-695-13
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```
Query Match 100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGCTTTTATATACTTAACCTTG 21
|||
Db 1 CTGCTTTTATATACTTAACCTTG 21
```

RESULT 6

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US-09-732-914-95/c
; Sequence 95, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attB0
US-09-732-914-95
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```
Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CTGCTTTTATATACTTAACCTTG 21
|||
Db 22 CTGCTTTTATATACTTAACCTG 2
```

RESULT 7

```
US-09-855-797A-60
; Sequence 60, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
```

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; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-60
```

```
Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGCTTTTATATACTTAACCTTG 21
|||
Db 4 CTGCTTTTATATACTTAACCTG 24
```

RESULT 8

```
US-09-907-900-60
; Sequence 60, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-60
```

```
Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGCTTTTATATACTTAACCTTG 21
|||
Db 4 CTGCTTTTATATACTTAACCTG 24
```

RESULT 9

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US-09-907-719-60
; Sequence 60, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
```

1 NUMBER OF SEQ ID NOS: 60
2 SOFTWARE: PatentIn Ver. 2.0
3 SEQ ID NO 60
4 LENGTH: 25
5 TYPE: DNA
6 ORGANISM: Unknown
7 FEATURE:
8 OTHER INFORMATION: Description of Unknown Organism: recombination
9 OTHER INFORMATION: Products
10 US-09-907-719-60

Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTACTTG 21
DB 4 CTGCTTTTATATACTACTTG 24

RESULT 10

US-09-432-085-31
1 Sequence 31, Application US/09432085
2 Publication No. US20030100110A1
3 GENERAL INFORMATION:
4 APPLICANT: Hartley, James L.
5 APPLICANT: Brasch, Michael A.
6 TITLE OF INVENTION: Recombinational Cloning Using Engineered
7 TITLE OF INVENTION: Recombination Sites
8 NUMBER OF SEQUENCES: 35
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
11 STREET: 1100 New York Ave., N. W. Suite 600
12 CITY: Washington
13 STATE: DC
14 COUNTRY: USA
15 ZIP: 20005-3934
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/432,085
23 FILING DATE: (Herewith)
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 09/233,493
27 FILING DATE: 20-JAN-1999
28 CLASSIFICATION:
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 09/005,476
31 FILING DATE: 12-JAN-1998
32 CLASSIFICATION:
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: 08/663,002
35 FILING DATE: 07-JUN-1995
36 CLASSIFICATION:
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: 08/486,139
39 FILING DATE: 07-JUN-1995
40 CLASSIFICATION:
41 TELECOMMUNICATION INFORMATION:
42 TELEPHONE: 202-371-2600
43 TELEFAX: 202-371-2540
44 INFORMATION FOR SEQ ID NO: 31:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 25 base pairs
47 TYPE: nucleic acid
48 STRANDEDNESS: both
49 TOPOLOGY: both
50 MOLECULE TYPE: cDNA
51 US-09-432-085-31

Query Match 100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTACTTG 21
DB 4 CTGCTTTTATATACTACTTG 24

RESULT 11

US-09-432-085-32/c
1 Sequence 32, Application US/09432085
2 Publication No. US20030100110A1
3 GENERAL INFORMATION:
4 APPLICANT: Hartley, James L.
5 APPLICANT: Brasch, Michael A.
6 TITLE OF INVENTION: Recombinational Cloning Using Engineered
7 TITLE OF INVENTION: Recombination Sites
8 NUMBER OF SEQUENCES: 35
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
11 STREET: 1100 New York Ave., N. W. Suite 600
12 CITY: Washington
13 STATE: DC
14 COUNTRY: USA
15 ZIP: 20005-3934
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/432,085
23 FILING DATE: (Herewith)
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 09/233,493
27 FILING DATE: 20-JAN-1999
28 CLASSIFICATION:
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 09/005,476
31 FILING DATE: 12-JAN-1998
32 CLASSIFICATION:
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: 08/663,002
35 FILING DATE: 07-JUN-1995
36 CLASSIFICATION:
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: 08/486,139
39 FILING DATE: 07-JUN-1995
40 CLASSIFICATION:
41 TELECOMMUNICATION INFORMATION:
42 TELEPHONE: 202-371-2600
43 TELEFAX: 202-371-2540
44 INFORMATION FOR SEQ ID NO: 32:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 25 base pairs
47 TYPE: nucleic acid
48 STRANDEDNESS: both
49 TOPOLOGY: both
50 MOLECULE TYPE: cDNA
51 US-09-432-085-32

Query Match 100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTACTTG 21
DB 22 CTGCTTTTATATACTACTTG 2

```

RESULT 12
US-09-985-448-60
; Sequence 60, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/985,448
; PRIOR FILING DATE: 1998-10-23
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-60

Query Match          100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
    |||||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 13
US-10-680-316-60
; Sequence 60, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-680-316-60

Query Match          100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
    |||||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 14
US-10-058-291-31
; Sequence 31, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/058,291
; APPLICATION NUMBER: US/10/058,291
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-058-291-31

Query Match          100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
    |||||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 15
US-10-058-291-32/c
; Sequence 32, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

```

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Db 4 CTGCTTTTATATACTAATTG 24

RESULT 14
US-10-058-291-31
; Sequence 31, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/058,291
; APPLICATION NUMBER: US/10/058,291
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
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Db 4 CTGCTTTTATATACTAATTG 24

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; Sequence 32, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 STREET: 1100 New York Ave., N. W. Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
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 FILING DATE: 30-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/432,085
 FILING DATE: 1999-11-02
 APPLICATION NUMBER: 09/233,493
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: 09/005,476
 FILING DATE: 12-JAN-1998
 APPLICATION NUMBER: 08/663,002
 FILING DATE: 07-JUN-1996
 APPLICATION NUMBER: 08/486,139
 FILING DATE: 07-JUN-1995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 32:
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 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
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 US-10-058-291-32

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 Db 22 CTGCTTTTATTAATACTTG 2

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 Job time : 27.5292 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 15:48:15 ; Search time 144.957 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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and is derived by analysis of the total score distribution.

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C 6	21	100.0	25	6	AR163203	AR163203 Sequence
C 7	21	100.0	25	6	BD263313	BD263313 Compositi
8	21	100.0	25	6	AX491670	AX491670 Sequence
9	21	100.0	25	6	AX498641	AX498641 Sequence
10	21	100.0	25	6	BD131386	BD131386 Recombina
11	21	100.0	26	6	AR142201	AR142201 Sequence
C 12	21	100.0	26	6	AR142202	AR142202 Sequence
13	21	100.0	27	6	A46167	A46167 Sequence 5
C 14	21	100.0	27	6	A46168	A46168 Sequence 6
15	21	100.0	27	6	AR361092	AR361092 Sequence
C 16	21	100.0	27	6	AR361093	AR361093 Sequence
17	21	100.0	27	6	AX787502	AX787502 Sequence
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C 26	21	100.0	1709	1	ECU39938	U39938 Escherichia
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C 40	21	100.0	5872	6	AR101810	AR101810 Sequence
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LOCUS AR265736 21 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 6 from patent US 6492164.
ACCESSION AR265736
VERSION AR265736.1 GI:29694577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Crouzet,J., Scherman,D., Cameron,B., Wils,P. and Darquet,A.-M.
TITLE Circular DNA expression cassettes for gene transfer
JOURNAL Patent: US 6492164-A 6 10-DEC-2002;
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LOCUS      AX092112          21 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116345.
ACCESSION  AX092112
VERSION     AX092112.1  GI:13444355
KEYWORDS   .
ORGANISM   Escherichia coli
SOURCE     Escherichia coli
REFERENCE  1
AUTHORS    Drooge,P.
TITLE      Sequence-specific dna recombination in eukaryotic cells
JOURNAL    Patent: WO 0116345-A 1 08-MAR-2001;
           Drooge, Peter (DE)
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DEFINITION Sequence 31 from patent US 6171861.
ACCESSION  ARI24551
VERSION     ARI24551.1  GI:14109912
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6171861-A 31 09-JAN-2001;
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DEFINITION Sequence 32 from patent US 6171861.
ACCESSION  ARI24552
VERSION     ARI24552.1  GI:14109913
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6171861-A 32 09-JAN-2001;
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DEFINITION Sequence 31 from patent US 6270969.
ACCESSION  ARI63202
VERSION     ARI63202.1  GI:16233722
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6270969-A 31 07-AUG-2001;
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DEFINITION Sequence 32 from patent US 6270969.
ACCESSION  ARI63203
VERSION     ARI63203.1  GI:16233725
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites

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JOURNAL Patent: US 6270969-A 32 07-AUG-2001;
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 DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
 ACCESSION BD263313.1 GI:33073081
 VERSION BD263313.1
 KEYWORDS JP 2002537790-A/91.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
 TITLE Compositions and methods for use in recombinational cloning of nucleic acids
 JOURNAL Patent: JP 2002537790-A 91 12-NOV-2002;
 COMMENT INVITROGEN CORP
 OS Artificial Sequence
 PN JP 2002537790-A/91
 PD 12-NOV-2002
 PE 02-MAR-2000 JP 2000602252
 PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
 28-MAY-1999 US 60/136744
 PT JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
 C12N15/09,C07K14/00,C12N1/19,C12N1/15,C12N1/21,C12N5/10,C12N15/ PC
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 Db 22 CTGCTTTTATATACTAACTTG 2

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 ACCESSION AX491670
 VERSION AX491670.1 GI:22324178
 KEYWORDS .
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1

AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1227147-A 31 31-JUL-2002;
 INVITROGEN CORPORATION (US)
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 DEFINITION Sequence 31 from Patent EP1229113.
 ACCESSION AX498641
 VERSION AX498641.1 GI:23343438
 KEYWORDS .
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1229113-A 31 07-AUG-2002;
 INVITROGEN CORPORATION (US)
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 Db 4 CTGCTTTTATATACTAACTTG 24

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 DEFINITION Recombinational cloning using nucleic acids having recombination sites.
 ACCESSION BD131386
 VERSION BD131386.1 GI:23226331
 KEYWORDS JP 2002500861-A/60.
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
 TITLE Recombinational cloning using nucleic acids having recombination sites
 JOURNAL Patent: JP 2002500861-A 60 15-JAN-2002;
 LIFE TECHNOLOGIES INC
 COMMENT OS Unknown
 PN JP 2002500861-A/60
 PD 15-JAN-2002
 PF 26-OCT-1998 JP 2000518069
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
 JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC

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C12N15/09, C1201/68, C12N15/00
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DEFINITION Sequence 7 from patent US 6174708.
ACCESSION ARI42201
VERSION ARI42201.1 GI:15102501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sodoyer, R., Aujame, L., Geoffroy, F. and Bouchardon, A.
TITLE Preparation of a multicombinatorial library of antibody gene
expression vectors
JOURNAL Patent: US 6174708-A 7 16-JAN-2001;
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QY 1 CTGCTTTTATATACTACTTG 21
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DEFINITION Sequence 8 from patent US 6174708.
ACCESSION ARI42202
VERSION ARI42202.1 GI:15102502
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sodoyer, R., Aujame, L., Geoffroy, F. and Bouchardon, A.
TITLE Preparation of a multicombinatorial library of antibody gene
expression vectors
JOURNAL Patent: US 6174708-A 8 16-JAN-2001;
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DEFINITION Sequence 5 from Patent WO9521914.
ACCESSION ARI42201
VERSION ARI42201.1 GI:2300415
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Sodoyer, R., Aujame, L. and Geoffroy, F.
TITLE METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
JOURNAL Patent: WO 9521914-A 5 17-AUG-1995;
COMMENT PASTEUR MERIEUX SERUMS VACC (FR)
Other publication AU 1666895 950829
Other publication FR 2715940 950811.
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DEFINITION Sequence 6 from Patent WO9521914.
ACCESSION ARI42202
VERSION ARI42202.1 GI:2300416
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Sodoyer, R., Aujame, L. and Geoffroy, F.
TITLE METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
JOURNAL Patent: WO 9521914-A 6 17-AUG-1995;
COMMENT PASTEUR MERIEUX SERUMS VACC (FR)
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GenCore version 5.1.6
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Maximum Match 100%

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SUMMARIES

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6	21	100.0	25	3	US-09-005-476-32
7	21	100.0	25	3	US-09-233-492-31
8	21	100.0	25	3	US-09-233-492-32
9	21	100.0	25	3	US-09-296-280-60
10	21	100.0	25	4	US-09-498-074-31
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12	21	100.0	25	5	PCT-US96-10082A-31
13	21	100.0	26	3	US-09-101-629A-7
14	21	100.0	26	3	US-09-101-629A-8
15	21	100.0	27	4	US-08-693-234-5
16	21	100.0	27	4	US-08-693-234-6
17	21	100.0	37	3	US-08-894-511-1
18	21	100.0	37	3	US-08-894-511-2
19	21	100.0	37	4	US-09-655-728-1
20	21	100.0	37	4	US-09-655-728-2
21	21	100.0	49	3	US-08-894-511-22
22	21	100.0	49	3	US-09-655-728-22
23	21	100.0	53	3	US-09-101-629A-10
24	21	100.0	55	3	US-09-101-629A-9
25	21	100.0	57	3	US-08-894-511-23
26	21	100.0	57	4	US-09-655-728-23
27	21	100.0	58	3	US-09-296-280-31

28 21 100.0 2321 3 US-09-198-839-2 Sequence 2, Appli
29 21 100.0 2321 4 US-09-562-834-2 Sequence 2, Appli
30 21 100.0 2321 4 US-09-395-396-2 Sequence 2, Appli
31 21 100.0 2337 3 US-09-198-839-3 Sequence 3, Appli
32 21 100.0 2337 4 US-09-562-834-3 Sequence 3, Appli
33 21 100.0 2337 4 US-09-395-396-3 Sequence 3, Appli
34 21 100.0 5872 3 US-08-411-768B-6 Sequence 1, Appli
35 21 100.0 5872 3 US-08-411-768B-6 Sequence 6, Appli
36 21 100.0 7652 1 US-07-590-988A-1 Sequence 1, Appli
37 19.4 92.4 228 4 US-09-107-532A-667 Sequence 667, App
38 19.4 92.4 1407 4 US-09-489-039A-5557 Sequence 5557, App
39 19.4 92.4 2408 1 US-08-486-013-69 Sequence 69, Appl
40 19.4 92.4 2408 2 US-08-482-279-69 Sequence 69, Appl
41 19.4 92.4 2408 2 US-08-342-268-69 Sequence 69, Appl
42 19.4 92.4 2408 3 US-09-015-968-69 Sequence 69, Appl
43 19.4 92.4 2408 4 US-09-397-386-69 Sequence 69, Appl
44 19.4 92.4 3484 4 US-09-308-090-1 Sequence 1, Appli
45 19.4 92.4 3484 4 US-09-380-090A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-894-511-6
; Sequence 6, Application US/08894511
; Patent No. 6143530
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: CAMERON, Beatrice
; APPLICANT: WILS, Pierre
; APPLICANT: DARQUET, Anne-Marie
; TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3c43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,511
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02117
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/00274
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST95013-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"

US-08-894-511-6

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
|||||
Db 1 CTGCTTTTATATACTAATTG 21

RESULT 2

US-09-655-728-6

; Sequence 6, Application US/09655728

; Patent No. 6492164

; GENERAL INFORMATION:

; APPLICANT: CROUZET, Joel

; SCHERMAN, Daniel

; CAMERON, Beatrice

; WILS, Pierre

; DARQUET, Anne-Marie

; TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
; USE THEREOF IN GENE THERAPY

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/655,728

; FILING DATE: 05-Sep-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/894,511

; FILING DATE: <Unknown>

; APPLICATION NUMBER: WO 98/00274

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky Esq., Martin F.

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: ST95013-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-3816

; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "Oligonucleotide"

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-655-728-6

Query Match 100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
|||||
Db 1 CTGCTTTTATATACTAATTG 21

RESULT 3

US-09-233-493-31

; Sequence 31, Application US/09233493

; Patent No. 6143557

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; TITLE OF INVENTION: Recombinational Cloning Using Engineered

; TITLE OF INVENTION: Recombination Sites

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

; STREET: 1100 New York Ave., N. W. Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/233,493

; FILING DATE: 20-JAN-1999

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 09/005,476

; FILING DATE: 12-JAN-1998

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/663,002

; FILING DATE: 07-JUN-1996

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/486,139

; FILING DATE: 07-JUN-1995

; CLASSIFICATION:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: cDNA

US-09-233-493-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
|||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 4

US-09-233-493-32/c

; Sequence 32, Application US/09233493

; Patent No. 6143557

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; TITLE OF INVENTION: Recombinational Cloning Using Engineered

; TITLE OF INVENTION: Recombination Sites

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

; STREET: 1100 New York Ave., N. W. Suite 600

; CITY: Washington

; STATE: DC

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;
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/233,493
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 5
US-09-005-476-31
; Sequence 31, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 6
US-09-005-476-32/c
; Sequence 32, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 7
US-09-233-492-31
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 4 CTGCTTTTATATACTTG 24

RESULT 6
US-09-005-476-32/c
; Sequence 32, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 7
US-09-233-492-31
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; Sequence 31, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-233-492-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
Db 4 CTGCTTTTATATACTAAGTTG 24

RESULT 8
US-09-233-492-32/c
; Sequence 32, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-233-492-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
Db 22 CTGCTTTTATATACTAAGTTG 2

RESULT 9
US-09-296-280-60
; Sequence 60, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-60

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
Db 4 CTGCTTTTATATACTAAGTTG 24
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RESULT 10
US-09-498-074-31
; Sequence 31, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-31

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21
Db 4 CTGCTTTTATATACTACTTG 24

RESULT 11
US-09-498-074-32/c
; Sequence 32, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-31

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21
Db 4 CTGCTTTTATATACTACTTG 24
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STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-32

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21
Db 22 CTGCTTTTATATACTACTTG 2

RESULT 12
PCT-US96-10082A-31
; Sequence 31, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-31

Query Match 100.0%; Score 21; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 4 CTGCTTTTATACAACTTG 24

RESULT 13

US-09-101-629A-7
; Sequence 7, Application US/09101629A
; Patent No. 6174708
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, Regis
; APPLICANT: Aujame, Luc
; APPLICANT: Geoffroy, Frederique
; APPLICANT: Bouchardon, Annabelle
; TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
; TITLE OF INVENTION: Gene Expression Vectors
; FILE REFERENCE: 98,381
; CURRENT APPLICATION NUMBER: US/09/101,629A
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: PCT/FR96/01938
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: FR 95 14 325
; PRIOR FILING DATE: 1995-12-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AttB Sph+
US-09-101-629A-7

Query Match 100.0%; Score 21; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAACTTG 21
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DB 2 CTGCTTTTATACAACTTG 22

RESULT 14

US-09-101-629A-8/c
; Sequence 8, Application US/09101629A
; Patent No. 6174708
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, Regis
; APPLICANT: Aujame, Luc
; APPLICANT: Geoffroy, Frederique
; APPLICANT: Bouchardon, Annabelle
; TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
; TITLE OF INVENTION: Gene Expression Vectors
; FILE REFERENCE: 98,381
; CURRENT APPLICATION NUMBER: US/09/101,629A
; CURRENT FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: PCT/FR96/01938
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: FR 95 14 325
; PRIOR FILING DATE: 1995-12-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AttB Sph-
US-09-101-629A-8

Query Match 100.0%; Score 21; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 21 CTGCTTTTATACAACTTG 1

RESULT 15

US-08-693-234-5
; Sequence 5, Application US/08693234
; Patent No. 6599697
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, ET AL
; TITLE OF INVENTION: PROCESS FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF VECTORS FOR
; TITLE OF INVENTION: EXPRESSING ANTIBODY GENES
; FILE REFERENCE: P03144US0/BAS
; CURRENT APPLICATION NUMBER: US/08/693,234
; CURRENT FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: PCT/FR95/00127
; PRIOR FILING DATE: 1995-02-02
; PRIOR APPLICATION NUMBER: FR 94 01519
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Escherichia coli
US-08-693-234-5

Query Match 100.0%; Score 21; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 3 CTGCTTTTATACAACTTG 23

Search completed: September 9, 2004, 21:21:16
Job time : 5.63035 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 ; Search time 169.634 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-1

Perfect score: 21

Sequence: 1 ctgtctttttataacttg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gssi:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	427	28	AQ990175 Rfc00900
2	21	100.0	450	28	AQ990483 Rfc01260
3	21	100.0	469	28	AQ990485 Rfc01263
4	21	100.0	517	28	AQ990287 Rfc01035

5	21	100.0	519	28	AQ990174
6	21	100.0	556	28	AQ991338
7	21	100.0	572	28	AQ989502
8	21	100.0	573	28	AQ991578
9	21	100.0	618	28	AQ991068
10	21	100.0	641	28	AQ990513
11	21	100.0	651	28	AQ990758
12	21	100.0	664	28	AQ991011
13	21	100.0	672	28	AQ990864
14	21	100.0	675	28	AQ991241
15	21	100.0	695	28	AQ991039
16	21	100.0	696	28	AQ991211
17	21	100.0	708	28	AQ990869
18	21	100.0	712	28	AQ990809
19	21	100.0	715	28	AQ991358
20	21	100.0	719	28	AQ991352
21	21	100.0	743	28	AQ990346
22	21	100.0	751	28	AQ989566
23	21	100.0	753	28	AQ990861
24	21	100.0	764	28	AQ990110
25	21	100.0	767	28	AQ990301
26	21	100.0	769	28	AQ990470
27	21	100.0	808	28	AQ990388
28	19.4	92.4	360	9	AU244794
29	19.4	92.4	417	12	BM134283
30	19.4	92.4	770	28	AQ991774
31	19.4	92.4	791	28	AQ991791
32	19.4	92.4	829	29	CC546560
33	19.4	92.4	909	13	BX329593
34	19.4	92.4	949	13	BX341052
35	19.4	92.4	962	9	AL526048
36	19.4	92.4	974	13	BX419333
37	19.4	92.4	1014	9	AL536199
38	19.4	92.4	1028	13	BX441494
39	19.4	92.4	1035	13	BX419222
40	19.4	92.4	1035	13	BX459157
41	19.4	92.4	1036	13	BX441486
42	19.4	92.4	1117	13	BX460736
43	19.4	92.4	1119	13	BX362060
44	19.4	92.4	1201	9	AL549604
45	19.4	92.4	1201	13	BX356247

ALIGNMENTS

RESULT 1

AQ990175

LOCUS

DEFINITION

AQ990175 427 bp DNA linear GSS 14-AUG-2000

Rfc00900 Photorhabdus luminescens strain W14 M13 library

Photorhabdus luminescens genomic clone PLG00900, genomic survey

sequence.

ACCESSION

AQ990175.1 GI:9648769

VERSION

AQ990175

KEYWORDS

GSS

SOURCE

Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 427)

french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,

Daborn,P.J., Bowen,D. and Blattner,F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

10919786

Contact: ffrench-Constant RH

Department of Biology and Biochemistry

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Tel: (44) 1225 826621

Fax: (44) 1225 826779

```

Email: bsrifc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
  1..427
  /organism="Photorhabdus luminescens"
  /mol_type="genomic DNA"
  /strain="W14"
  /db_xref="taxon:29488"
  /clone="PLG00900"
  /dev_stage="primary phase variant"
  /clone_lib="Photorhabdus luminescens strain W14 M13
  library"
  /note="Genomic DNA from strain W14 was size selected (1-2
  kb) and then cloned into M13 Janus."

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  Best Local Similarity 100.0%; Pred. No. 5.7e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  CTGCTTTTATACTAATTG 21
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Db   21  CTGCTTTTATACTAATTG 41

RESULT 2
AQ990483
LOCUS
DEFINITION
  AQ990483 450 bp DNA linear GSS 14-AUG-2000
  Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01260, genomic survey
  sequence.
ACCESSION
  AQ990483
VERSION
  AQ990483.1 GI:9649077
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 450)
  AUTHORS
    french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
    Daborn,P.J., Bowen,D. and Blattner,F.R.
  TITLE
    A genomic sample sequence of the entomopathogenic bacterium
    Photorhabdus luminescens W14: potential implications for virulence
    Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
  JOURNAL
  MEDLINE
  PUBMED
  COMMENT
    Contact: french-Constant RH
    Department of Biology and Biochemistry
    University of Bath
    South Building, Bath BA2 7AY, UK
    Tel: (44) 1225 826621
    Fax: (44) 1225 826779
    Email: bsrifc@bath.ac.uk
    This is one of 2,122 random reads from the M13 library. For
    annotation of identified clones (BLASTX, BLASTN and mapping to E.
    coli K12 genome) please see french-Constant et al. 2000, Nucleic
    Acids Res.
    Seq primer: M13 Forward
    Class: shotgun.
    Location/Qualifiers
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      /organism="Photorhabdus luminescens"
      /mol_type="genomic DNA"
      /strain="W14"
      /db_xref="taxon:29488"
      /clone="PLG01260"
      /dev_stage="primary phase variant"
      /clone_lib="Photorhabdus luminescens strain W14 M13
      library"
      /note="Genomic DNA from strain W14 was size selected (1-2
      kb) and then cloned into M13 Janus."

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  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   19  CTGCTTTTATACTAATTG 39

RESULT 3
AQ990485
LOCUS
DEFINITION
  AQ990485 469 bp DNA linear GSS 14-AUG-2000
  Rfc01263 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01263, genomic survey
  sequence.
ACCESSION
  AQ990485
VERSION
  AQ990485.1 GI:9649079
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 469)
  AUTHORS
    french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
    Daborn,P.J., Bowen,D. and Blattner,F.R.
  TITLE
    A genomic sample sequence of the entomopathogenic bacterium
    Photorhabdus luminescens W14: potential implications for virulence
    Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
  JOURNAL
  MEDLINE
  PUBMED
  COMMENT
    Contact: french-Constant RH
    Department of Biology and Biochemistry
    University of Bath
    South Building, Bath BA2 7AY, UK
    Tel: (44) 1225 826621
    Fax: (44) 1225 826779
    Email: bsrifc@bath.ac.uk
    This is one of 2,122 random reads from the M13 library. For
    annotation of identified clones (BLASTX, BLASTN and mapping to E.
    coli K12 genome) please see french-Constant et al. 2000, Nucleic
    Acids Res.
    Seq primer: M13 Forward
    Class: shotgun.
    Location/Qualifiers
      1..469
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      /mol_type="genomic DNA"
      /strain="W14"
      /db_xref="taxon:29488"
      /clone="PLG01263"
      /dev_stage="primary phase variant"
      /clone_lib="Photorhabdus luminescens strain W14 M13
      library"
      /note="Genomic DNA from strain W14 was size selected (1-2
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  Best Local Similarity 100.0%; Pred. No. 5.5e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   27  CTGCTTTTATACTAATTG 47

RESULT 4
AQ990287

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LOCUS
DEFINITION Rfc01035 Photorhabdus luminescens strain W14 M13 library GSS 14-AUG-2000
Photobhabdus luminescens genomic clone PLG01035, genomic survey
sequence.

ACCESSION
VERSION AQ990287
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 517)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.

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source
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Location/Qualifiers
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/dev_stage="primary phase variant"
/clone="PLG01035"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 100.0%; Score 21; DB 28; Length 517;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
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Db 30 CTGCTTTTATATACTAATTG 50

RESULT 5
AQ990174
LOCUS
DEFINITION Rfc00899 Photorhabdus luminescens strain W14 M13 library GSS 14-AUG-2000
Photobhabdus luminescens genomic clone PLG00899, genomic survey
sequence.

ACCESSION
VERSION AQ990174
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 519)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.

JOURNAL
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.

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/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 100.0%; Score 21; DB 28; Length 519;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
|||||
Db 21 CTGCTTTTATATACTAATTG 41

RESULT 6
AQ991338
LOCUS
DEFINITION Rfc02255 Photorhabdus luminescens strain W14 M13 library GSS 14-AUG-2000
Photobhabdus luminescens genomic clone PLG02255, genomic survey
sequence.

ACCESSION
VERSION AQ991338
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 556)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.

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FEATURES
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        /organism="Photorhabdus luminescens"
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        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match      100.0%; Score 21; DB 28; Length 556;
  Best Local Similarity 100.0%; Pred. No. 5.3e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTACTAATTG 21
Db 20 CTGCTTTTATTACTAATTG 40

RESULT 7
AQ989502
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Rf000051 Photorhabdus luminescens genomic clone PLG00051, genomic survey
  sequence.
ACCESSION
  AQ989502.1 GI:9648096
VERSION
  AQ989502
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 572)
  ffrench-Constant R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
10919786
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssr@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
  Location/Qualifiers
    1..572
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      /mol_type="genomic DNA"
      /strain="W14"
      /db_xref="taxon:29488"
      /clone="PLG02569"
      /dev_stage="primary phase variant"
      /clone_lib="Photorhabdus luminescens strain W14 M13 library"
      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 5.2e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTACTAATTG 21
Db 31 CTGCTTTTATTACTAATTG 51

RESULT 9
AQ991068
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Rf001926 Photorhabdus luminescens genomic clone PLG01926, genomic survey
  sequence.
ACCESSION
  AQ991068.1 GI:9649662
VERSION
  AQ991068
KEYWORDS
  GSS.

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SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 618)

AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE
20378633

PUBMED
10919786

COMMENT
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Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers
1..618
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTTAACCTG 21
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22 CTGCTTTTATATACTTAACCTG 42

Db

RESULT 10
AQ990513

LOCUS
AQ990513.1 GI:9649107

DEFINITION
Photorhabdus luminescens strain W14 M13 library

ACCESSION
AQ990513

VERSION
AQ990513.1 GI:9649107

KEYWORDS
GSS.

SOURCE
Photorhabdus luminescens

ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 641)

AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE
20378633

PUBMED
10919786

COMMENT
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South Building, Bath BA2 7AY, UK

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Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers
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/organism="Photorhabdus luminescens"
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/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

Query Match 100.0%; Score 21; DB 28; Length 641;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTTAACCTG 21
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26 CTGCTTTTATATACTTAACCTG 46

Db

RESULT 11
AQ990758

LOCUS
AQ990758.1 GI:9649352

DEFINITION
Photorhabdus luminescens strain W14 M13 library

ACCESSION
AQ990758

VERSION
AQ990758.1 GI:9649352

KEYWORDS
GSS.

SOURCE
Photorhabdus luminescens

ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
1 (bases 1 to 651)

AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE
20378633

PUBMED
10919786

COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers
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/clone="PLG01579"

FEATURES
source

/dev stage="primary phase variant"
/clone lib="Photorhabdus luminescens strain W14 M13
library"
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kb) and then cloned into M13 Janus."

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
|||||
Db 28 CTGCTTTTATTAAGTACTTG 48

RESULT 12
AQ991011
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Rf021864 Photorhabdus luminescens genomic clone PLG01864, genomic survey
sequence.

ACCESSION AQ991011 GI:9649605
VERSION AQ991011.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens

REFERENCE 1 (bases 1 to 654)
AUTHORS ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786

COMMENT Contact: ffrrench-Constant RH
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.

FEATURES

source
Location/Qualifiers
1..654
/organism="Photorhabdus luminescens"
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
|||||
Db 29 CTGCTTTTATTAAGTACTTG 49

RESULT 13
AQ990864
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Rf021701 Photorhabdus luminescens genomic clone PLG01701, genomic survey
sequence.

ACCESSION AQ990864 GI:9649458
VERSION AQ990864.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens

REFERENCE 1 (bases 1 to 672)
AUTHORS ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786

COMMENT Contact: ffrrench-Constant RH
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Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.

FEATURES

source
Location/Qualifiers
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/organism="Photorhabdus luminescens"
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/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 21; DB 28; Length 672;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
|||||
Db 29 CTGCTTTTATTAAGTACTTG 49

RESULT 14
AQ991241
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Rf021332 Photorhabdus luminescens genomic clone PLG02132, genomic survey
sequence.

ACCESSION AQ991241 GI:9649835
VERSION AQ991241.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens

REFERENCE 1 (bases 1 to 675)
AUTHORS ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrrench-Constant RH
 Department of Biology and Biochemistry
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 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
 Acids Res.

Seq primer: M13 Forward
 Class: shotgun.
 FEATURES source
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 /clone_lib="Photorhabdus luminescens strain W14 M13
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 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 21; DB 28; Length 675;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
 |||||
 Db 28 CTGCTTTTATTAATACTTG 48

RESULT 15
 AQ991039
 LOCUS 695 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rfc01894 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01894, genomic survey
 sequence.
 ACCESSION AQ991039.1 GI:9649633
 VERSION AQ991039
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 695)
 ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrrench-Constant RH
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 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
 Acids Res.

Seq primer: M13 Forward
 Class: shotgun.
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 /mol_type="genomic DNA"
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 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
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ORIGIN

Query Match 100.0%; Score 21; DB 28; Length 695;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
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QY 1 CTGCTTTTATTAATACTTG 21
 |||||
 Db 30 CTGCTTTTATTAATACTTG 50

Search completed: September 9, 2004, 21:18:21
 Job time : 171.634 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11 ; Search time 53.5798 Seconds
(without alignments)
2516.866 Million cell updates/sec

Title: US-10-082-772B-2
Perfect score: 243
Sequence: 1 tctgttacagggtcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	243	100.0	6043	4	US-09-630-929-4
C 3	243	100.0	7652	1	US-07-590-988A-1
4	144	59.3	201	1	US-08-021-667A-18
5	144	59.3	201	1	US-08-410-544-18
6	144	59.3	201	1	US-08-728-785A-18
7	104.6	43.0	38584	4	US-09-453-702B-50
8	100.4	41.3	2408	1	US-08-486-013-69
9	100.4	41.3	2408	2	US-08-482-279-69
10	100.4	41.3	2408	2	US-08-342-268-69
11	100.4	41.3	2408	3	US-09-015-968-69
12	100.4	41.3	2408	4	US-09-397-386-69
13	100.4	41.3	3484	4	US-09-308-090-1
14	100.4	41.3	3484	4	US-09-380-090A-1
15	100.4	41.3	3757	2	US-09-016-366A-13
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C 18	100.4	41.3	5611	4	US-09-068-101-10
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21	97.4	40.1	200	1	US-08-728-785A-17
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23	78.6	32.3	228	4	US-09-107-532A-667
24	45.8	18.8	640681	4	US-09-790-988-1
25	44.6	18.4	7786	4	US-09-790-988-2
26	41.6	17.1	10467	4	US-10-204-708-2
27	41	16.9	3078	4	US-09-601-198-54

28	40	16.5	408	4	US-09-621-976-8544	Sequence 8544, Ap
C 29	40	16.5	4185	4	US-09-417-485D-7	Sequence 7, Appli
C 30	39.6	16.3	732	4	US-09-134-000C-2779	Sequence 2779, Ap
31	39.6	16.3	6866	4	US-10-204-708-19	Sequence 19, Appl
32	39.2	16.1	3680	4	US-09-647-390-15	Sequence 15, Appl
33	39.2	16.1	6768	1	US-08-107-755A-1	Sequence 1, Appli
34	39.2	16.1	8457	1	US-07-991-867B-1	Sequence 1, Appli
35	39.2	16.1	8457	2	US-08-544-332-1	Sequence 1, Appli
36	39.2	16.1	8457	4	US-09-370-861A-1	Sequence 13, Appl
C 37	39.2	16.1	19124	2	US-08-487-826B-13	Sequence 33, Appl
C 38	39	16.0	1117	3	US-09-247-373B-33	Sequence 3, Appli
39	39	16.0	10619	4	US-10-204-708-3	Sequence 38, Appl
C 40	38.8	16.0	1048	4	US-09-489-847-38	Sequence 39, Appl
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42	38.6	15.9	1151	1	US-08-236-754-3	Sequence 1, Appli
43	38.6	15.9	3055	1	US-08-236-754-1	Patent No. 5231168
C 44	38.6	15.9	3095	6	5231168-1	Sequence 89, Appl
45	38.6	15.9	5844	4	US-10-204-708-89	

ALIGNMENTS

RESULT 1
US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Query Match 100.0%; Score 243; DB 3; Length 4909;
Best Local Similarity 100.0%; Pred. No. 9.8e-45;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTTACAGTCACTAATCACTAGTTCATGCTGATGCTGATGCTG 60
|||||

Db 2516 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTGTG 2457
 QY 61 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 120
 Db 2456 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 2397
 QY 121 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 180
 Db 2396 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 2337
 QY 181 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 240
 Db 2336 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 2277
 QY 241 TTC 243
 Db 2276 TTC 2274

RESULT 2
 US-09-630-929-4/c
 ; Sequence 4, Application US/09630929
 ; Patent No. 6620585
 ; GENERAL INFORMATION:
 ; APPLICANT: Judith W. Zyskind
 ; TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
 ; FILE REFERENCE: ELTRA.012A
 ; CURRENT APPLICATION NUMBER: US/09/630,929
 ; CURRENT FILING DATE: 2000-08-02
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 6043
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi
 ; OTHER INFORMATION: sequences inserted
 US-09-630-929-4

Query Match 100.0%; Score 243; DB 4; Length 6043;
 Best Local Similarity 100.0%; Pred. No. 9.9e-45;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTGTG 60
 Db 5414 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTGTG 5355
 QY 61 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 120
 Db 5354 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 5295
 QY 121 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 180
 Db 5294 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 5235
 QY 181 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 240
 Db 5234 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 5175
 QY 241 TTC 243
 Db 5174 TTC 5172

RESULT 3
 US-07-590-988A-1
 ; Sequence 1, Application US/07590988A
 ; Patent No. 5227288
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; TITLE OF INVENTION: DNA Sequencing Vector with

; TITLE OF INVENTION: Reversible Insert
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Quarles and Brady
 ; STREET: P.O. BOX 2113
 ; CITY: MADISON
 ; STATE: WISCONSIN
 ; COUNTRY: U.S.A.
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh
 ; SOFTWARE: Microsoft Word 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/590,988A
 ; FILING DATE: 19901001
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nicholas J. Seay
 ; REGISTRATION NUMBER: 27,386
 ; REFERENCE/DOCKET NUMBER: 9629691682
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 251-5000
 ; TELEFAX: (608) 251-9166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7652 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: Other nucleic acid;
 ; DESCRIPTION: synthetic recombinant plasmid
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; US-07-590-988A-1
 Query Match 100.0%; Score 243; DB 1; Length 7652;
 Best Local Similarity 100.0%; Pred. No. 1e-44;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTGTG 60
 Db 5933 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTGTG 5992
 QY 61 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 120
 Db 5993 TTTTACAGTATTATGATGCTGTTTATGCAAAATCTAATTAATATATGATATTTA 6052
 QY 121 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 180
 Db 6053 TATCATTTTACGTTTCTCGTTGAGCTTTTATGCAAAATCTAATTAATATATGATATTTA 6112
 QY 181 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 240
 Db 6113 GCTTATCAATTTGTTGCAACGACGTCACATCATGTCAGTCAAAATCTAATTAATATATGATATTTA 6172
 QY 241 TTC 243
 Db 6173 TTC 6175

RESULT 4
 US-08-021-667A-18
 ; Sequence 18, Application US/08021667A
 ; Patent No. 5434049
 ; GENERAL INFORMATION:
 ; APPLICANT: Okano, Kazunori
 ; APPLICANT: Kambara, Hideki
 ; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
 ; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
 ; TITLE OF INVENTION: METHOD USING SAME

```
;/ NUMBER OF SEQUENCES: 18
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Antonelli, Terry, Stout & Kraus
;/ STREET: Suite 600, 1919 Pennsylvania Ave., NW
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20006
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/021,667A
;/ FILING DATE: 19930224
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Terry, David T.
;/ REGISTRATION NUMBER: 20,178
;/ REFERENCE/DOCKET NUMBER: 520.31930X00
;/ TELEPHONE: 202-828-0300
;/ TELEFAX: 202-828-0380
;/ TELEX: 440280/248545
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 201 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ HYPOTHETICAL: YES
;/ ANTI-SENSE: NO
;/ US-08-021-667A-18

Query Match 59.3%; Score 144; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AATTGAATATTGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATATACTAAG 159
Db 1 AATTGAATATTGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATATACTAAG 60
QY 160 TTGGCATTATAAAAGCATTGCTTATCATTAATTTGTCACGACGACAGGTCACTATCAGTC 219
Db 61 TTGGCATTATAAAAGCATTGCTTATCATTAATTTGTCACGACGACAGGTCACTATCAGTC 120
QY 220 AAAATAAAATCAATTTGATTTC 243
Db 121 AAAATAAAATCAATTTGATTTC 144

RESULT 5
US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/410,544
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION NUMBER: 08/021,667
;/ FILING DATE: 24-FEB-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Terry, David T.
;/ REGISTRATION NUMBER: 20,178
;/ REFERENCE/DOCKET NUMBER: 520.31930X00
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-828-0300
;/ TELEFAX: 202-828-0380
;/ TELEX: 248545
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 201 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ HYPOTHETICAL: YES
;/ ANTI-SENSE: NO
;/ US-08-410-544-18

Query Match 59.3%; Score 144; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AATTGAATATTGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATATACTAAG 159
Db 1 AATTGAATATTGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATATACTAAG 60
QY 160 TTGGCATTATAAAAGCATTGCTTATCATTAATTTGTCACGACGACAGGTCACTATCAGTC 219
Db 61 TTGGCATTATAAAAGCATTGCTTATCATTAATTTGTCACGACGACAGGTCACTATCAGTC 120
QY 220 AAAATAAAATCAATTTGATTTC 243
Db 121 AAAATAAAATCAATTTGATTTC 144

RESULT 6
US-08-728-785A-18
; Sequence 18, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
```

ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION:

FILING
ATTORNEY/AGENCY

```

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-486-013-69

Query Match 41.3%; Score 100.4; DB 1; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 9
US-08-482-279-69
; Sequence 69, Application US/08482279
; Patent No. 5840498
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,279
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,279
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-482-279-69

Query Match 41.3%; Score 100.4; DB 2; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 11
US-09-015-968-69

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Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 10
US-08-342-268-69
; Sequence 69, Application US/08342268
; Patent No. 5844072
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,268
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-342-268-69

Query Match 41.3%; Score 100.4; DB 2; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 11
US-09-015-968-69

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; Sequence 69, Application US/09015968
; Patent No. 6057425
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,968
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,279
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-015-968-69

Query Match 41.3%; Score 100.4; DB 3; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 408 CTGCTTTTATCTAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGTTGTTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGTTGTTTC 509

RESULT 12
US-09-397-386-69
; Sequence 69, Application US/09397386
; Patent No. 6300470
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use

; Sequence 69, Application US/09308090
; Patent No. 6395963
; GENERAL INFORMATION:
; APPLICANT: Ohl, Stephan
; APPLICANT: Van Der Lee, Frederique
; APPLICANT: Goddijn, Oscar
; APPLICANT: Klap, Joke
; APPLICANT: Sijmons, Peter
; TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
; FILE REFERENCE: MOG 57680
; CURRENT APPLICATION NUMBER: US/09/308,090
; CURRENT FILING DATE: 1999-05-14
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;
; EARLIER APPLICATION NUMBER: PCT/EP97/06472
; EARLIER FILING DATE: 1997-11-18
; EARLIER APPLICATION NUMBER: EP 96203213.2
; EARLIER FILING DATE: 1996-11-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3484
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3482)..(3484)
; US-09-308-090-1

Query Match      41.3%; Score 100.4; DB 4; Length 3484;
Best Local Similarity 99.0%; Pred. No. 9.9e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 201
Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 202 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 243
Db 480 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 521

RESULT 14
US-09-380-090A-1
; Sequence 1, Application US/09380090A
; Patent No. 6555529
; GENERAL INFORMATION:
; APPLICANT: OHL, Stephan Andreas
; SIMONS, Peter Christiaan
; KLEIN-VAN DER LEE, Frederique
; Marianne
; GODDIN, Oscar
; KLAEP, Joke
; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
; SEQUENCES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,090A
; FILING DATE: 17-May-1999
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06472
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: EP 96203213.2
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: SYN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3484 base pairs
```

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;
;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; STRAIN: C24
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3481..3484
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-380-090A-1

Query Match      41.3%; Score 100.4; DB 4; Length 3484;
Best Local Similarity 99.0%; Pred. No. 9.9e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 201
Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 202 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 243
Db 480 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 521

RESULT 15
US-09-016-366A-13
; Sequence 13, Application US/09016366A
; Patent No. 5953431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3757 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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US-09-016-366A-13

	Query Match	41.3%	Score 100.4;	DB 2;	Length 3757;
	Best Local Similarity	99.0%;	Pred. No. 9.9e-14;		
	Matches 101;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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Db	374	CTGCTTTTTTATCTAAAGTTGGCATTTATAAAAAAGCATTCGCTTATCAATTTGTGCAACG	433		
Qy	202	AACAGGTCACATCAAGTCAAAAATAAATCATTTATTTGATTTTC	243		
Dd	434	AACAGGTCACATCAAGTCAAAAATAAATCATTTATTTGATTTTC	475		

Search completed: September 9, 2004, 21:21:18
Job time : 55.5798 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 15:48:15 ; Search time 1677.36 Seconds
(without alignments)
6279.120 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

Sequence: 1 ttgttacaggcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.cm.*

5: gb.ov.*

6: gb.pat.*

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8: gb.pl.*

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34: em.htg_pln.*

35: em.htg_rod.*

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37: em.htg_vrt.*

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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	100.0	243	6	AX092113	Sequence
2	243	100.0	361	7	LAMINTATT	M23841 Bacterioph
3	243	100.0	610	6	AX101000	AX101000 Sequence
4	243	100.0	1668	9	MACHSS	D85521 Macaca fasc
5	243	100.0	1763	6	BD225932	BD225932 Immediate
6	243	100.0	2758	3	PEAHPCC	M17028 P.falciparu
7	243	100.0	3485	12	AF178449	AF178449 Integrati
8	243	100.0	3485	12	AF178450	AF178450 Integrati
9	243	100.0	4105	12	AF271663	AF271663 Cloning v
10	243	100.0	4190	12	XXU13848	U13848 pExCell cto
11	243	100.0	4549	12	AF178452	AF178452 Integrati
12	243	100.0	4549	12	AF178453	AF178453 Integrati
13	243	100.0	5641	6	AX113748	AX113748 Sequence
14	243	100.0	5670	6	AX113749	AX113749 Sequence
15	243	100.0	5826	6	AX113746	AX113746 Sequence
16	243	100.0	6000	12	U66308	U66308 Expression
17	243	100.0	6043	6	AR399301	AR399301 Sequence
18	243	100.0	6043	6	AX370644	AX370644 Sequence
19	243	100.0	6071	6	AX113747	AX113747 Sequence
20	243	100.0	7176	12	AF178451	AF178451 Integrati
21	243	100.0	42529	12	CVU39284	U39284 Cloning vec
22	243	100.0	42530	12	CVU39285	U39285 Cloning vec
23	243	100.0	42531	12	CVU39286	U39286 Cloning vec
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28	231	95.1	3663	12	AY048716	AY048716 CRIM plas
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30	231	95.1	4782	12	AY048740	AY048740 CRIM plas
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32	231	95.1	5739	12	AY054372	AY054372 CRIM plas
33	231	95.1	5771	12	AY150262	AY150262 CRIM plas
34	231	95.1	5771	12	AY150263	AY150263 CRIM plas
35	231	95.1	5814	12	AY150265	AY150265 CRIM plas
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37	231	95.1	5948	12	AY054373	AY054373 CRIM plas
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39	231	95.1	6200	12	AY150266	AY150266 CRIM plas
40	231	95.1	6664	12	AY048713	AY048713 CRIM plas
41	231	95.1	6668	12	AY048714	AY048714 CRIM plas
42	231	95.1	6742	12	AY048739	AY048739 CRIM plas
43	226.8	93.3	4165	6	BD263380	BD263380 Compositi
44	226.8	93.3	4204	6	BD263378	BD263378 Compositi
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ALIGNMENTS

RESULT 1	AX092113	AX092113	243 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	Sequence 2 from Patent WO0116345.					
DEFINITION	AX092113					
ACCESSION	AX092113					
VERSION	AX092113.1	GI:13444356				
KEYWORDS						
SOURCE	Bacteriophage lambda					
ORGANISM	Bacteriophage lambda					
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;					
AUTHORS	Lambda-like viruses.					
TITLE	Droege, P.					
JOURNAL	Sequence-specific dna recombination in eukaryotic cells					
	Patent: WO 0116345-A 2 08-MAR-2001;					

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QY 241 TTC 243
Db 241 TTC 243

RESULT 2
LAMINTATT/c
LOCUS      LAMINTATT      361 bp      DNA      linear      PHG 28-APR-1993
DEFINITION Bacteriophage lambda int gene region.
ACCESSION M23841
VERSION M23841.1 GI:215177
KEYWORDS site-specific recombination.
SOURCE Bacteriophage lambda
ORGANISM Bacteriophage lambda
REFERENCE 1 (bases 1 to 361)
AUTHORS Schmeissner,U., McKenney,K., Rosenberg,M. and Court,D.
TITLE Removal of a terminator structure by RNA processing regulates int gene expression
JOURNAL J. Mol. Biol. 176 (1), 39-53 (1984)
MEDLINE 84242838
PUBMED 6234400
COMMENT Original source text: Bacteriophage lambda DNA.
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QY 1 TCTGTTACAGTCACTAATACCATCTAAAGTAGTGTGATTCATAGTCACTGCATATCTGTG 60
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QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
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Db 181 GCTTATCAATTTGTTGCAACGAGGTCACCTATCAGTCAAAATATAAATCAATTTTGTAT 240
QY 241 TTC 243
Db 241 TTC 243

RESULT 3
LOCUS      AX101000
DEFINITION Sequence 1 from Patent WO0121780.
ACCESSION AX101000
VERSION AX101000.1 GI:13619857
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
REFERENCE 1
AUTHORS Meyer,P.L. and Zubko,E.L.
TITLE Targeted gene removal.
JOURNAL Patent: WO 0121780-A 1 29-MAR-2001;
        THE UNIVERSITY OF LEEDS (GB)
FEATURES
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QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
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Db 259 TATCATTTTACGTTTCTGCTGCTTTTATCTAGTGTGATTTTATCTAGTGTGATTTA 318
QY 181 GCTTATCAATTTGTTGCAACGAGGTCACCTATCAGTCAAAATATAAATCAATTTTGTAT 240
Db 319 GCTTATCAATTTGTTGCAACGAGGTCACCTATCAGTCAAAATATAAATCAATTTTGTAT 378
QY 241 TTC 243
Db 379 TTC 381

RESULT 4
LOCUS      MACHSS/c
DEFINITION MACHSS fascicularis mRNA for hydroxysteroid sulfotransferase
ACCESSION D85521
VERSION D85521.1 GI:1345405
KEYWORDS hydroxysteroid sulfotransferase subunit.
SOURCE MACHSS fascicularis (crab-eating macaque)
ORGANISM MACHSS fascicularis
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
        Cercopithecinae; Macaca.

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REFERENCE 1 (bases 1 to 1668)
AUTHORS Ogura,K., Satsukawa,M., Kato,K., Okuda,H. and Watabe,T.
TITLE Molecular cloning of monkey liver hydroxysteroid sulfotransferase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1668)
AUTHORS Ogura,K.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Pharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518,
Fax:+81-426-76-4517)
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QY 61 TTTTACAGTATTATAGTCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 120
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Db 271 TATCATTTTACGTTCTCGTTTCAGCTTTTATATCTAAGTTGGCAATTAATAAAAGCAAT 212
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QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATAAATCATTTATTTGAT 240
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QY 241 TTC 243
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Db 151 TTC 149
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RESULT 5
BD225932/c
LOCUS BD225932 1763 bp DNA linear PAT 17-JUL-2003
DEFINITION Immediate early gene and method for using the same.
ACCESSION BD225932
VERSION BD225932.1 GI:33035702
KEYWORDS JP 2002512772-A/49.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1763)
AUTHORS Worley,P.F., Lanahan,A., Goetz,B., Hiemisch,H., Kuner,R.,

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Scheek,S., Nikolich,K. and Zhukovski,E.
Immediate early gene and method for using the same
Patent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
BIOSCIENCE AG
OS Rattus norvegicus (rat)
PN JP 2002512772-A/49
PD 08-MAY-2002
PF 05-FEB-1999 JP 2000530634
PR 09-FEB-1998 US 60/074135,12-FEB-1998 US 60/074518 PT
PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI
ROHINI KUNER.
PI SIGRID SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC
C12N15/09,A61K31/711,A61K48/00,A61P25/00,A61P25/28,C07H21/04, PC
C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/08 PC
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PC C12N15/00,C12N5/00
CC n is either a, t, g, or c
FH Key Location/Qualifiers
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RESULT 6
PEAHRPC/c
LOCUS PEAHRPC 2758 bp DNA linear INV 26-APR-1993
DEFINITION P.falciiparum histidine-rich protein genes.
ACCESSION M17028
VERSION M17028.1 GI:160339
KEYWORDS histidine-rich protein.
SOURCE Plasmodium falciiparum (malaria parasite P. falciiparum)
ORGANISM Plasmodium falciiparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 2758)
AUTHORS Lenstra,R., d'Auric,I., Andrieu,B., Le Bras,J. and Galibert,F.
TITLE Cloning and sequencing of Plasmodium falciiparum DNA fragments
containing repetitive regions potentially coding for histidine-rich
proteins: identification of two overlapping reading frames
JOURNAL Biochem. Biophys. Res. Commun. 146 (1), 368-377 (1987)
MEDLINE 87270765
PUBMED 3038111
COMMENT Original source text: P.falciiparum, cDNA to mRNA, clone M4.
FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.2e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 TTC 243
Db 913 TTC 915

RESULT 9
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DEFINITION Integration vector pCDL1PSK chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178450
VERSION AF178450.1 GI:9294788
KEYWORDS Integration vector pCDL1PSK
SOURCE Integration vector pCDL1PSK
ORGANISM Artificial sequences; vectors.
REFERENCE 1 (bases 1 to 3485)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL Plasmid 43 (1), 12-23 (2000)
MEDLINE 20079288
PUBMED 10610816
REFERENCE 2 (bases 1 to 3485)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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Db 853 GCTTATCAATTTGTTGCAACAGAGTCATATCACTCAAGTCAAAATATAAATCAATTTTAT 240

QY 241 TTC 243
Db 913 TTC 915

RESULT 9
AF271663 LOCUS 4105 bp DNA circular SYN 11-JUL-2000
DEFINITION Cloning vector pLDR9, complete sequence.
ACCESSION AF271663
VERSION AF271663.1 GI:9022390
KEYWORDS Cloning vector pLDR9
SOURCE Cloning vector pLDR9
ORGANISM Artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4105)
AUTHORS Wiencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and
August,P.R.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA
FEATURES
source
1..4105
Location/Qualifiers
/organism="Cloning vector pLDR9"
/mol_type="genomic DNA"
/db_xref="taxon:130501"
216..1031
/ function="confers kanamycin resistance"
/ codon_start=1
/ transl_table=11
/ product="aminoglycoside 3' phosphotransferase"
/ protein_id="AAF82363.1"
/ db_xref="GI:9022392"
/ translation="MSHIQETSCSRPLNSMDADLYGKYKWARDNVGSGATYRLY
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GKPAPELXLKHGKGVANDVTDEMVRNLNLTETMPLTLIKHFIETPDAMLLTTAIP
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 1528..2388

CDS

/EC number="3.5.2.6"
 /note="derived from pMWB66EH"

/codon_start=1
 /transl_table=11

/product="beta-lactamase"
 /protein_id="AAF82362.1"

/db_xref="GI:9022391"

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 DRWPELNEAIPNDERDTPMVAMATTIKLLTGELLTLASRQQLIDWMDKVGAPL
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CDS

complement(1992..2258)

/note="hypothetical 9.2 kD protein"

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misc_feature

2612..2859

/note="attP"

ORIGIN

Query Match 100.0%; Score 243; DB 12; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 5e-34; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTGAATGATGTTGG 60

Db 2617 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTGAATGATGTTGG 2676

QY 61 TTTTACAGTATATAGTAGTCGCTTTTATGCAAAATCTAATTTAATATATGATTTA 120

Db 2677 TTTTACAGTATATAGTAGTCGCTTTTATGCAAAATCTAATTTAATATATGATTTA 2736

QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATGCAAAATCTAATTTAATATATGATTTA 180

Db 2737 TATCATTTTACGTTCTCGTTCAGCTTTTATGCAAAATCTAATTTAATATATGATTTA 2796

QY 181 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTATTTGAT 240

Db 2797 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTATTTGAT 2856

QY 241 TTC 243

Db 2857 TTC 2859

RESULT 10

XXU13848/C

LOCUS XXU13848 4190 bp DNA circular SYN 13-DEC-1994

DEFINITION pEXcell cloning vector, complete sequence.

ACCESSION U13848

VERSION U13848.1 GI:595702

KEYWORDS T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide, attP.

SOURCE unidentified cloning vector

ORGANISM unidentified cloning vector

REFERENCE 1 (bases 1 to 4190)

AUTHORS Malone, J.A.

TITLE lambda ExCell: A multifunctional cloning vector that is released from

JOURNAL lambda ExCell by in vivo excision

REFERENCE 2 (bases 1 to 4190)

AUTHORS

Direct Submission

TITLE

Submitted (19-AUG-1994) James A. Malone, International Technical
 Services, Molecular Biology Reagents Division, Pharmacia Biotech
 Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA

JOURNAL

FEATURES

source

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/organism="unidentified cloning vector"

/mol_type="genomic DNA"

/db_xref="taxon:45196"

/lab_host="Escherichia coli"

34..894

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34..894

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/transl_table=11

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/db_xref="GI:595704"

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 DRWPELNEAIPNDERDTPMVAMATTIKLLTGELLTLASRQQLIDWMDKVGAPL
 LRSALPAGWFIADKSGAGERSGRIIAALGPDGKSRIVVIYTTGSAQTMDERNRQIA
 BIGASLIKHW"

1653

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/direction=right

2001..2033

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2001..2007

/gene="lac"

/note="lac promoter"

2013..2033

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2051..2209

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/db_xref="GI:595703"

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2073..2089

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2073..2089

/gene="SP6 RNA polymerase"

2097..2154

/note="Multiple Cloning Site (MCS); contains unique sites
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complement(2155..2174)

complement(2155..2174)

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 the first base of the newly synthesized single strand"

/direction=right

3847..4094

/gene="attP"

3847..4094

/gene="attP"

/note="attP gene from lambda"

3932..3947

/gene="attP"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACTGATCATATGTTGTG 60
Db 4089 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACTGATCATATGTTGTG 4030

QY 61 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 120
Db 4029 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 3970

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAATGTTGGCATTATATAAAAGCATT 180
Db 3969 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAATGTTGGCATTATATAAAAGCATT 3910

QY 181 GCATTATCAATTTGTTGCAAGCAAGTCATCTACGTCAAAATATAAATCATTTATTTGAT 240
Db 3909 GCATTATCAATTTGTTGCAAGCAAGTCATCTACGTCAAAATATAAATCATTTATTTGAT 3850

QY 241 TTC 243
Db 3849 TTC 3847

RESULT 11
AF178452
LOCUS      4549 bp      DNA      linear      SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
            and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178452
VERSION   AF178452.1 GI:9294794
KEYWORDS  .
SOURCE    Integration vector pCD13PKS
ORGANISM  Integration vector pCD13PKS
            artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4549)
AUTHORS  Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE    Genetic system for reversible integration of DNA constructs and
            lacZ gene fusions into the Escherichia coli chromosome
JOURNAL  Plasmid 43 (1), 12-23 (2000)
MEDLINE  20079288
PUBMED   10610816
REFERENCE 2 (bases 1 to 4549)
AUTHORS  Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE    Direct Submission
JOURNAL  Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
            Science I Building, Ames, IA 50011, USA
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CDS        complement(1798..2652)
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Best Local Similarity 100.0%; Pred. No. 4.9e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACTGATCATATGTTGTG 60
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QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAATGTTGGCATTATATAAAAGCATT 180
Db 793 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAATGTTGGCATTATATAAAAGCATT 852

QY 181 GCATTATCAATTTGTTGCAAGCAAGTCATCTACGTCAAAATATAAATCATTTATTTGAT 240
Db 853 GCATTATCAATTTGTTGCAAGCAAGTCATCTACGTCAAAATATAAATCATTTATTTGAT 912

QY 241 TTC 243
Db 913 TTC 915

RESULT 12
AF178453
LOCUS      4549 bp      DNA      linear      SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
            and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178453
VERSION   AF178453.1 GI:9294797
KEYWORDS  .
SOURCE    Integration vector pCD13PKS
ORGANISM  Integration vector pCD13PKS
            artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4549)
AUTHORS  Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE    Genetic system for reversible integration of DNA constructs and
            lacZ gene fusions into the Escherichia coli chromosome
JOURNAL  Plasmid 43 (1), 12-23 (2000)
MEDLINE  20079288
PUBMED   10610816
REFERENCE 2 (bases 1 to 4549)
AUTHORS  Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE    Direct Submission
JOURNAL  Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
            Science I Building, Ames, IA 50011, USA
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misc_feature 668..915
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CDS complement(1798..2652)
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BHSVALGPAPELFDVPPEQDLFEALNETLTLWNSPPDWAGDERNVLTLSRWYSA
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gene complement(3818..4201)
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Best Local Similarity 100.0%; Pred. No. 4.9e-34;
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Db 673 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATTCATAGTCGATGATGTTG 732
QY 61 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 120
Db 733 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 792
QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
Db 793 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 852
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATATAATCATTATTGAT 240
Db 853 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATATAATCATTATTGAT 912
QY 241 TTC 243
Db 913 TTC 915

RESULT 13
AX113748
LOCUS AX113748 5641 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 13 from Patent WO0127322.
ACCESSION AX113748
VERSION AX113748.1 GI:13939915
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Zyskind, J.
TITLE Chitobiose as a reporter enzyme
JOURNAL Patent: WO 0127322-A 13 19-APR-2001;
Elitra Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers

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Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4703 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATTCATAGTCGATGATGTTG 4762
QY 61 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 120
Db 4763 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 4822
QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
Db 4823 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 4882
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATATAATCATTATTGAT 240
Db 4883 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATATAATCATTATTGAT 4942
QY 241 TTC 243
Db 4943 TTC 4945

RESULT 14
AX113749/c
LOCUS AX113749 5670 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 14 from Patent WO0127322.
ACCESSION AX113749
VERSION AX113749.1 GI:13939916
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Zyskind, J.
TITLE Chitobiose as a reporter enzyme
JOURNAL Patent: WO 0127322-A 14 19-APR-2001;
Elitra Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..5670
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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 4.7e-34;
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Db 5041 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATTCATAGTCGATGATGTTG 4982
QY 61 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 120
Db 4981 TTTTACAGTATATAGTCTGCTGTTTATGCAAAATCTAATTTAATATATGATTTA 4922
QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
Db 4921 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 4862
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATATAATCATTATTGAT 240

Db 4861 GCTTATCAATTTCTGCAACGACAGTGCTATCATCAGTCAAAATAAAATCATTATTGAT 4802
 QY 241 TTC 243
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 Db 4801 TTC 4799

RESULT 15
 AX113746
 LOCUS AX113746 5826 bp DNA linear PAT 01-MAY-2001
 DEFINITION Sequence 11 from Patent WO0127322.
 ACCESSION AX113746
 VERSION AX113746.1 GI:13939913
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Zyskind J.
 TITLE Chitobiase as a reporter enzyme
 JOURNAL Patent: WO 0127322-A 11 19-APR-2001;
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="pDYK9"

ORIGIN
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 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 4888 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTGAAGTGCATATGTTGTG 4947
 QY 61 TTTTACAGTATTATGATGCTGTTTTTTTATGCAAAATCTAATTTAATATATATGATATTTA 120
 Db 4948 TTTTACAGTATTATGATGCTGTTTTTTTATGCAAAATCTAATTTAATATATATGATATTTA 5007
 QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 180
 Db 5008 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 5067
 QY 181 GCTTATCAATTTGTTGCAACGACAGTGCTATCATCAGTCAAAATAAAATCATTATTGAT 240
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 QY 241 TTC 243
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 Db 5128 TTC 5130

Search completed: September 9, 2004, 19:34:29
 Job time : 1679.36 secs

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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 ; Search time 276.724 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	100.0	243	4 AAF61418	Aaf61418 Bacteriop
2	243	100.0	248	8 ACC85316	Acc85316 Recombina
3	243	100.0	282	7 ACC44676	Acc44676 Murine rD
4	243	100.0	282	7 ABT16636	Abt16636 Artificia
5	243	100.0	610	5 AAF79770	Aaf79770 Bacteriop
6	243	100.0	1469	7 ABQ80306	Abq80306 Lambda fr
7	243	100.0	1469	7 ACC83020	Acc83020 Bacteriop
8	243	100.0	1763	2 AAZ30709	Aaz30709 Rat neuro
9	243	100.0	4346	7 ACC44716	Acc44716 Plasmid p
10	243	100.0	4346	7 ABT16615	Abt16615 Artificia
11	243	100.0	4909	2 AAT18924	Aat18924 Plasmid p
12	243	100.0	5641	4 AAF30800	Aaf30800 Vector pl
13	243	100.0	5670	4 AAF30801	Aaf30801 Vector pl
14	243	100.0	5826	4 AAF30798	Aaf30798 Vector pl
15	243	100.0	6071	4 AAF30799	Aaf30799 Vector pl
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17	241.4	99.3	243	4 AAF61421	Aaf61421 E. coli a
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21	226.8	93.3	4470	3 AAC55521	Aac55521 Donor pla
22	226.8	93.3	4470	7 ABZ58767	Abz58767 Destinati
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	31	226.6	93.3	233	7 ACC59568	Acc59568 Nucleic a
	32	226.6	93.3	233	3 AAC55522	Aac55522 Donor pla
c	33	225.4	92.8	4204	3 AAC55523	Aac55523 Donor pla
	34	225.4	92.8	4208	7 ABZ58768	Abz58768 Destinati
	35	225.4	92.8	4428	7 ABZ58768	Abz58768 Destinati
	36	225.4	92.8	4470	3 AAC55521	Aac55521 Donor pla
	37	225.4	92.8	4470	7 ABZ58767	Abz58767 Destinati
	38	225.4	92.8	4627	7 ABZ58769	Abz58769 Destinati
	39	225.4	92.8	4892	8 ADA50329	Ada50329 Plasmid v
	40	225.4	92.8	4939	3 AAC55525	Aac55525 Donor pla
c	41	225.4	92.8	5584	3 AAC55632	Aac55632 Donor pla
	42	225.4	92.8	5584	7 ABZ58766	Abz58766 Donor pla
c	43	225.2	92.7	4165	3 AAC55524	Aac55524 Donor pla
c	44	225.2	92.7	5156	3 AAC55526	Aac55526 Donor pla
c	45	225	92.6	233	3 AAC55383	Aac55383 Recombina

ALIGNMENTS

RESULT 1
AAF61418
ID AAF61418 standard; DNA; 243 BP.
XX
AC AAF61418;
XX
DT 05-JUN-2001 (first entry)
XX
DE Bacteriophage lambda attP DNA fragment.
XX
KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
KW targeted integration; attP; ds.
XX
OS Bacteriophage lambda.
XX
BN DE19941186-Al.
XX
PD 01-MAR-2001.
XX
PF 30-AUG-1999; 99DE-01041186.
XX
PR 30-AUG-1999; 99DE-01041186.
XX
PA (DROE/) DROEGE P.
XX
PI Droege P;
XX
DR WPI; 2001-246016/26.
XX
PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
PT for somatic cell gene therapy, uses an integrase to effect recombination
PT between att sites.
XX
PS Claim 2; Page 13; 24pp; German.
XX
CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (1) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC vector containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences
XX

CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an Aves. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of Aves comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 7; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.8e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCTGACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATGTTGTG 60
 DB |||||
 QY 15 TCCTGACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATGTTGTG 74
 DB |||||
 QY 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 120
 DB |||||
 QY 75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 134
 DB |||||
 QY 121 TATCATTTTACGTTCTCGTTACGTTCTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 180
 DB |||||
 QY 135 TATCATTTTACGTTCTCGTTACGTTCTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 194
 DB |||||
 QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTTAAATATATTGATATTTA 240
 DB |||||
 QY 195 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTTAAATATATTGATATTTA 254
 DB |||||
 QY 241 TTC 243
 DB 255 TTC 257

RESULT 4
 ABT16636
 ID ABT16636 standard; DNA; 282 BP.
 XX
 AC ABT16636;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Artificial plant chromosome related oligo SEQ ID No 48.
 XX
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW Blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 XX
 PN W0200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 XX 30-MAY-2002; 2002WO-US017451.
 PF
 XX 30-MAY-2001; 2001US-0294687P.
 PR
 XX 04-JUN-2001; 2001US-0296329P.
 XX
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 DR WPI; 2003-140436/13.
 XX

PT Producing artificial chromosome by introducing a nucleic acid into plant
 PT cell, selecting artificial chromosome that has one or more repeat regions
 XX with equivalent amounts of euchromatic and heterochromatic nucleic acids.
 PS Disclosure; Page 263-264; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product.
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention
 XX
 SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 7; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.8e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCTGACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATGTTGTG 60
 DB |||||
 QY 15 TCCTGACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATGTTGTG 74
 DB |||||
 QY 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 120
 DB |||||
 QY 75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 134
 DB |||||
 QY 121 TATCATTTTACGTTCTCGTTACGTTCTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 180
 DB |||||
 QY 135 TATCATTTTACGTTCTCGTTACGTTCTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 194
 DB |||||
 QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTTAAATATATTGATATTTA 240
 DB |||||
 QY 195 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTTAAATATATTGATATTTA 254
 DB |||||
 QY 241 TTC 243
 DB 255 TTC 257

RESULT 5
 AAF79770
 ID AAF79770 standard; DNA; 610 BP.
 XX
 AC AAF79770;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Bacteriophage lambda attachment P region.
 XX
 KW Attachment P region; attP; recombination; marker gene removal; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN W0200121780-A2.
 XX
 PD 29-MAR-2001.
 XX
 DR 15-SEP-2000; 2000WO-GH003543.
 XX

PR 17-SEP-1999; 99GB-00021937.
 XX (UYLE-) UNIV LEEDS.
 XX Meyer P, Zubko R;
 XX WPI; 2001-266072/27.
 XX Removing a part of a transgene which has been integrated into a genome
 PT comprises inducing intrachromosomal homologous recombination between the
 PT attachment P regions of bacteriophage lambda flanking the transgene.
 XX
 XX Claim 8; Fig 3D; 25pp; English.
 XX
 CC The present invention describes a method of removing a transgene marker
 CC by flanking the transgene with a bacteriophage lambda attachment P (attP)
 CC region and inducing homologous recombination between attP regions so that
 CC the transgene is removed. This is useful in the production of transgenic
 CC plants with less risk of inter-species transmission of marker genes
 CC which often encode proteins associated with, for example, herbicide and
 CC antibiotic resistance. The present sequence is the attP coding region
 XX
 SQ Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
 Query Match 100.0%; Score 243; DB 5; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCATATGTTG 60
 Db 139 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCATATGTTG 198
 QY 61 TTTTACAGTATATGATGCTCTGTTTTATGCAAAATCTAATTTAATATGATTTA 120
 Db 139 TTTTACAGTATATGATGCTCTGTTTTATGCAAAATCTAATTTAATATGATTTA 258
 QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATACCTAAGTTCGTCATTATAAAAAGCATT 180
 Db 259 TATCATTTTACGTTTCTCGTTTCAGCTTTTATACCTAAGTTCGTCATTATAAAAAGCATT 318
 QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATAAATCATTTTGTAT 240
 Db 319 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATAAATCATTTTGTAT 378
 QY 241 TTC 243
 Db 379 TTC 381
 RESULT 6
 ABQ80306
 ID ABQ80306 standard; DNA; 1469 BP.
 XX
 AC ABQ80306;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Lambda fragment in plasmid DNA.
 XX
 XX Primer; PCR; amplify; lambda phage; primer material; insertion; SNP;
 KW deletion; single nucleotide polymorphism; sequencing; diagnosis; ss.
 OS Synthetic.
 XX
 FN WO2003027991-A1.
 XX
 XX 03-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-JP009766.
 XX
 PR 25-SEP-2001; 2001JP-00291249.
 XX
 XX (DNAF-) DNAFORM KK.

PA (RIKE) RIKEN KK.
 XX Hayashizaki Y;
 XX WPI; 2003-354676/33.
 XX Printed material useful as a delivery and storage system for oligomer
 PT and/or polymer, comprises a support having an oligomer and/or polymer
 PT applied on it.
 XX
 XX Example 1; Page 31-32; 91pp; English.
 XX
 CC The sequences given in ABQ80304-05 are primers which were used to amplify
 CC DNA for use in the material of the invention. The primers amplify a 1377
 CC bp portion of lambda phage DNA contained in a plasmid. The amplified
 CC sequence (ABQ80306) was attached to the primer material of the invention
 CC which comprises at least one support having at least one oligomer and/or
 CC polymer applied on it. The printed material is useful in a method for
 CC synthesising DNA where the product of amplification and/or ligation is
 CC cDNA and/or full-length cDNA which is recovered and used for
 CC determination of nucleotide insertion/deletion, single nucleotide
 CC polymorphism (SNP) and sequencing analysis, in a diagnostic method for
 CC determination of nucleotide insertion/deletion, or SNP analysis.
 CC Optionally, the cDNA and/or full-length cDNA is useful for the peptide,
 CC polypeptide or protein expression. The printed material is useful in
 CC research applications, or for providing scientists with oligomer and/or
 CC polymers from the printed materials easily and immediately. From the
 CC printed material, at least an oligomer and/or polymer can be obtained
 CC immediately and directly, without need to make a request for it. The
 CC oligomers and/or polymers can be delivered and stored easily with reduced
 CC labour and time while eliminating the need to use special equipment or
 CC facilities. Thus, the printed material is a quick, efficient and
 CC inexpensive sample delivery system
 XX
 SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 Query Match 100.0%; Score 243; DB 7; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCATATGTTG 60
 Db 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCATATGTTG 867
 QY 61 TTTTACAGTATATGATGCTCTGTTTTATGCAAAATCTAATTTAATATGATTTA 120
 Db 868 TTTTACAGTATATGATGCTCTGTTTTATGCAAAATCTAATTTAATATGATTTA 927
 QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATACCTAAGTTCGTCATTATAAAAAGCATT 180
 Db 928 TATCATTTTACGTTTCTCGTTTCAGCTTTTATACCTAAGTTCGTCATTATAAAAAGCATT 987
 QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATAAATCATTTTGTAT 240
 Db 988 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAGTCAAAATAAATCATTTTGTAT 1047
 QY 241 TTC 243
 Db 1048 TTC 1050
 RESULT 7
 ACC83020
 ID ACC83020 standard; DNA; 1469 BP.
 XX
 AC ACC83020;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
 XX
 KW Oligomer storage; oligomer delivery; ds.
 XX

OS Bacteriophage lambda.
 XX W02003040360-A1.
 XX
 XX PD 15-MAY-2003.
 XX
 XX PF 05-NOV-2002; 2002WO-JP011492.
 XX
 XX PR 05-NOV-2001; 2001JP-00339217.
 XX
 XX PA (RIKE) RIKEN KK.
 XX PA (DNAF-) DNAFORM KK.
 XX PA (HAYA/) HAYASHIZAKI Y.
 XX
 XX PI Hayashizaki Y;
 XX
 XX DR WPI; 2003-441569/41.
 XX
 XX PT New support useful for storing and/or delivering an oligomer and/or
 PT polymer applied on support, has oligomer and/or polymer applied on it,
 PT and a loose-leaf sheet or a card.
 XX
 XX PS Example 1; Page 30-31; 70pp; English.
 XX
 XX CC The invention relates to a method for storing and/or delivering an
 CC oligomer and/or polymer applied on support. The support has oligomer
 CC and/or polymer applied on it, and is in the form of loose-leaf sheet or a
 CC card. The support is useful for storing and/or delivering an oligomer
 CC and/or polymer applied on it. The present sequence is Bacteriophage
 CC lambda DNA used in the exemplification of the invention
 XX
 XX SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 243; DB 7; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATTTGTG 60
 Db 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATTTGTG 867
 QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 120
 Db 868 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 927
 QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATTAAGTGGCATTTAAAAAGCATT 180
 Db 928 TATCATTTTACGTTCTCGTTCAGCTTTTATTAAGTGGCATTTAAAAAGCATT 987
 QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTTGTAT 240
 Db 988 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTTGTAT 1047
 QY 241 TTC 243
 Db 1048 TTC 1050
 RESULT 8
 AAZ30709/c
 ID AAZ30709 standard; cDNA; 1763 BP.
 XX
 XX AC AAZ30709;
 XX
 XX DT 05-JAN-2000 (first entry)
 XX
 XX DE Rat neuronal immediate early gene cDNA clone R280.
 XX
 XX KW Immediate early gene; IEG; neuron; brain; function; growth factor;
 KW transcription factor; signal transduction; cytoskeletal protein;
 KW metabolic enzyme; learning; memory; synaptic transmission; tolerance;
 KW neuronal plasticity; ds.
 XX

OS Rattus sp.
 XX
 XX FN W09940225-A1.
 XX
 XX PD 12-AUG-1999.
 XX
 XX PF 05-FEB-1999; 99WO-US002462.
 XX
 XX PR 09-FEB-1998; 98US-0074135P.
 XX PR 12-FEB-1998; 98US-0074518P.
 XX
 XX PA (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PA (BADI) BASF-LYNX BIOSCIENCE AG.
 XX
 XX PI Worley PF, Lanahan A, Goetz B, Hiemisch H, Kuner R, Scheek S;
 XX PI Nikolich K, Zhukovski E;
 XX
 XX DR WPI; 1999-590697/50.
 XX
 XX PT Novel genes and polypeptides, useful for treating conditions related to a
 PT deficiency in nIEG responsiveness to a stimulus.
 XX
 XX PS Claim 1; Page 114-115; 134pp; English.
 XX
 XX CC This sequence represents rat neuronal immediate early gene (IEG) cDNA
 CC clone R280. An IEG is a gene whose expression is rapidly increased
 CC immediately following a stimulus e.g., neuronal stimulation. Such
 CC neuronal IEGs have been found to encode a variety of proteins, including
 CC transcription factors, cytoskeletal proteins, growth factors and
 CC metabolic enzymes, as well as proteins involved in signal transduction.
 CC The identification of neuronal IEGs and the proteins they encode may
 CC provide important information about the function of neurons in, for
 CC example, learning, memory, synaptic transmission, tolerance and neuronal
 CC plasticity. Neuronal IEGs, and antibodies against neuronal IEG proteins can
 CC be used to treat an animal with a deficiency in neuronal IEG responsiveness
 CC to stimuli, such that the effect of the deficiency is minimised. The
 CC deficiency may be a reduced or elevated level of expression of an IEG.
 CC The neuronal stimulus comprises a maximal electroconvulsive seizure and
 CC its effects influence learning or memory. The IEGs and protein products
 CC are useful in identifying compounds that modulate the expression or
 CC activity of IEG nucleic acids or proteins, respectively
 XX
 XX SQ Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
 SQ
 Query Match 100.0%; Score 243; DB 2; Length 1763;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATTTGTG 60
 Db 431 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATGATTTGTG 372
 QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 120
 Db 371 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 312
 QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATTAAGTGGCATTTAAAAAGCATT 180
 Db 311 TATCATTTTACGTTCTCGTTCAGCTTTTATTAAGTGGCATTTAAAAAGCATT 252
 QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTTGTAT 240
 Db 251 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTTGTAT 192
 QY 241 TTC 243
 Db 191 TTC 189
 RESULT 9
 ACC44716
 ID ACC44716 standard; DNA; 4346 BP.

Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 60
Db 4070 TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4129

QY 61 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
Db 4130 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA 4189

QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATATATAAAGCAATT 180
Db 4190 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATATATAAAGCAATT 4249

QY 181 GCTTATCAATTTGTTGCAACGACAGGTCATATCAGTCATCAAAATCAATATTTATGAT 240
Db 4250 GCTTATCAATTTGTTGCAACGACAGGTCATATCAGTCATCAAAATCAATATTTATGAT 4309

QY 241 TTC 243
Db 4310 TTC 4312

RESULT 11
AAT18924/c
ID AAT18924 standard; DNA; 4909 BP.

XX AC AAT18924;
XX DT 17-JAN-1997 (first entry)
XX DE Plasmid pA126i.
XX KW Spider; dragline protein; variant; monomer; polymer; circular;
XX KW fibre forming region; Spidroin 1; Nephila clavipes; Dp1; mimic;
XX KW DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope;
XX KW surgical suture; implant; reinforcement; film; coating; ss.
XX OS Synthetic.
XX PN WO9429450-A2.
XX PD 22-DEC-1994.
XX PF 15-JUN-1994; 94WO-US006689.
XX PR 15-JUN-1993; 93US-00077600.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Fahnstock SR;
XX DR WP1; 1995-036479/05.
XX PT New synthetic variants of spider dragline protein - for making fibres
XX PT useful as clothing, surgical silk, plastic reinforcement etc., also
XX PT related DNA, vectors and transformed cells.
XX PS Example 1; Fig 13; 169pp; English.
XX CC This sequence represents the complete nucleotide sequence of the plasmid
XX CC pA126i. This plasmid was used in the construction of the vector pPF510
XX CC which was used to express synthetic spider dragline variants, DP-1A.9 and
XX CC DP-1B.9. pA126i comprises a replication origin active in E. coli, a
XX CC selectable genetic marker which is a gene conferring resistance to
XX CC ampicillin, sites for the restriction endonucleases BamHI and BglII with
XX CC no essential sequences between them, and a third restriction site for
XX CC PstI, located within the selectable marker which produces cohesive ends
XX CC incompatible with those produced by BamHI and BglII. The polypeptide
XX CC monomers are variants based on a consensus sequence derived from the
XX CC fibre forming regions of spider dragline protein, esp. the natural
XX CC protein 1 (Spidroin 1) from Nephila clavipes. Synthetic analogues of Dp1

CC were designed to mimic the repeating consensus sequence of the natural
CC protein and the pattern of variation among individual repeats. DP-1A
CC analogues are composed of a tandemly repeated 101 amino acid monomer
CC which comprises four repeats which differ from the consensus sequence
CC given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine
CC sequence varies in length from 0-7 residues; (2) when the entire poly-
CC alanine sequence is deleted, so also is the surrounding sequence
CC encompassing AGGGGGGAGGAGG; (3) aside from the poly-alanine sequence,
CC deletions usually encompass integral multiples of three consecutive
CC residues; (4) deletion of GYG is generally accompanied by deletion of GRG
CC in the same sequence; and (5) a repeat in which the entire poly-alanine
CC sequence is deleted is generally preceded by a repeat containing six
CC alanine residues. The proteins may be used to produce fibres of high
CC tensile strength and elasticity, suitable for clothing, rope, surgical
CC sutures, biomaterials for implants, plastic reinforcements, films,
CC coatings, etc
XX SQ Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 2; Length 4909;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 60
Db 2516 TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457

QY 61 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
Db 2456 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA 2397

QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATATATAAAGCAATT 180
Db 2396 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATATATAAAGCAATT 2337

QY 181 GCTTATCAATTTGTTGCAACGACAGGTCATATCAGTCATCAAAATCAATATTTATGAT 240
Db 2336 GCTTATCAATTTGTTGCAACGACAGGTCATATCAGTCATCAAAATCAATATTTATGAT 2277

QY 241 TTC 243
Db 2276 TTC 2274

RESULT 12
AAF30800
ID AAF30800 standard; DNA; 5641 BP.

XX AC AAF30800;
XX DT 11-SEP-2003 (revised)
XX DT 21-JUN-2001 (first entry)
XX DE Vector plasmid pJMF3 encoding LacZ-chitinase fusion.
XX KW Chitinase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
XX OS Escherichia coli.
XX OS Vibrio harveyi.
XX OS Bacteriophage lambda.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT protein_bind 1783..1810
XX FT /*tag= a
XX FT /*note= "CAP-cAMP binding site"
XX FT 1820..1826
XX FT /*tag= b
XX FT /*function= "Lac promoter"
XX FT 1845..1850
XX FT /*tag= c
XX FT /*function= "Lac promoter"
XX FT protein_bind 1857..1883

```
FT      /*tag= d
FT      /note= "Lac repressor binding site"
FT      1895..2014
FT      /*tag= e
FT      /partial
FT      /product= "lacZ-chitobiase fusion"
XX
XX WO200127322-A2.
XX
XX 19-APR-2001.
XX
XX 02-AUG-2000; 2000WO-US021048.
XX
XX 13-OCT-1999; 99US-0159221P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Zyskind J;
XX
XX WPI; 2001-290731/30.
XX P-PSDB; AAB20484.
XX
XX Identifying a regulatory element capable of directing or regulating
XX transcription (e.g. a promoter) comprises providing a construct linked to
XX a nucleic acid encoding a cytoplasmic form of chitobiase.
XX
XX Example 1; Page 32-34; 44pp; English.
XX
XX The present sequence is that of vector plasmid pJMF3, which includes
XX phage lambda attP and the lac promoter with the first 21 amino acids of
XX lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi
XX chitobiase gene (see AAB20484). The invention relates to genetic
XX constructs and methods of using a cytoplasmic form of chitobiase enzyme
XX as a reporter. A claimed reporter gene construct comprises pJMF3. The
XX invention also comprises expression vectors which express the cytoplasmic
XX form of chitobiase. Methods are provided for: characterizing a promoter;
XX identifying a regulatory element capable of directing and regulating
XX transcription within a test sequence; detecting a successful
XX transformation; and for monitoring the activity of a promoter. Chitobiase
XX has an advantage over beta-galactosidase as a reporter gene in that it is
XX not necessary to engineer many host cells to lack reporter activity.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 243; DB 4; Length 5641;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCTGTACAGGTCACCTAATACCATCTAAGTACTGATTCATAGTGCATGATGTTGG 60
XX Db |||||
XX 4703 TCTGTTACAGGTCACCTAATACCATCTAAGTACTGATTCATAGTGCATGATGTTGG 4762
XX
XX QY 61 TTTTACAGTATTATGATGATCTGTTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 120
XX Db |||||
XX 4763 TTTTACAGTATTATGATGATCTGTTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 4822
XX
XX QY 121 TATCATTTTACGTTTCTCGTTGAGCTTTTATATACATGATGTCATATAAAAACGATT 180
XX Db |||||
XX 4823 TATCATTTTACGTTTCTCGTTGAGCTTTTATATACATGATGTCATATAAAAACGATT 4882
XX
XX QY 181 GCTTATCAATTTGTTGCAAGACAGTCACTATCATGTCATAAATAAATCAATTTTGTAT 240
XX Db |||||
XX 4883 GCTTATCAATTTGTTGCAAGACAGTCACTATCATGTCATAAATAAATCAATTTTGTAT 4942
XX
XX QY 241 TTC 243
XX Db |||
XX 4943 TTC 4945
XX
XX RESULT 13
XX AAF30801/c
XX ID AAF30801 standard; DNA; 5670 BP.
```

```
XX AAF30801;
AC
XX 11-SEP-2003 (revised)
XX 21-JUN-2001 (first entry)
XX
XX Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
XX
XX Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
XX
XX Escherichia coli.
XX Vibrio harveyi.
XX Bacteriophage lambda.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX protein_bind 1783..1810
XX /*tag= a
XX /note= "CAP-cAMP binding site"
XX -35_signal 1820..1826
XX /*tag= b
XX -10_signal 1845..1850
XX /*tag= c
XX /function= "Lac promoter"
XX protein_bind 1857..1883
XX /*tag= d
XX /note= "Lac repressor binding site"
XX CDS 1895..2014
XX /*tag= e
XX /partial
XX /product= "lacZ-chitobiase fusion"
XX
XX WO200127322-A2.
XX
XX 19-APR-2001.
XX
XX 02-AUG-2000; 2000WO-US021048.
XX
XX 13-OCT-1999; 99US-0159221P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Zyskind J;
XX
XX WPI; 2001-290731/30.
XX P-PSDB; AAB20484.
XX
XX Identifying a regulatory element capable of directing or regulating
XX transcription (e.g. a promoter) comprises providing a construct linked to
XX a nucleic acid encoding a cytoplasmic form of chitobiase.
XX
XX Example 1; Page 34-36; 44pp; English.
XX
XX The present sequence is that of vector plasmid pJMF4, which includes
XX phage lambda attP and the lac promoter with the first 21 amino acids of
XX lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi
XX chitobiase gene (see AAB20484). The invention relates to genetic
XX constructs and methods of using a cytoplasmic form of chitobiase enzyme
XX as a reporter. A claimed reporter gene construct comprises pJMF4. The
XX invention also comprises expression vectors which express the cytoplasmic
XX form of chitobiase. Methods are provided for: characterizing a promoter;
XX identifying a regulatory element capable of directing and regulating
XX transcription within a test sequence; detecting a successful
XX transformation; and for monitoring the activity of a promoter. Chitobiase
XX has an advantage over beta-galactosidase as a reporter gene in that it is
XX not necessary to engineer many host cells to lack reporter activity.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 243; DB 4; Length 5670;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-40;
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Matches	243;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TCTGTTACAGGTCACTAATAACCATTAAAGTAGTGGATTCATAGTGACTGCATATGTTGTG	60						
Dd	5041	TCGTTTACAGGTCACIATAATACCATCTPAAGTAGTGGATTCATAGTGACTGCATATGTTGTG	4982						
Qy	61	TTTTACAGTAATATGTAAGTCGTGTTTTTATGCAAAAATCTAATTAATATATGATATTTA	120						
Dd	4981	TTTTACAGTAATATGTAAGTCGTGTTTTTATGCAAAAATCTAATTAATATATGATATTTA	4922						
Qy	121	TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCATTATAAAAAGCATT	180						
Dd	4921	TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCATTATAAAAAGCATT	4862						
Qy	181	GCTTATCAAATTTGTTGCAAGAACAGGTCCACTATFACGTCAAAATATAAATCATTTTGTAT	240						
Dd	4861	GCTTATCAAATTTGTTGCAAGAACAGGTCCACTATFACGTCAAAATATAAATCATTTTGTAT	4802						
Qy	241	TTT C 243							
Dd	4801	TTT C 4799							
 RESULT 14									
AAF30798									
ID	AAF30798 standard; DNA; 5826 BP.								
XX	AAF30798;								
XX									
DT	11-SEP-2003 (revised)								
DT	21-JUN-2001 (first entry)								
XX									
DE	Vector plasmid pDYK6 encoding chitobiase reporter enzyme.								
XX									
KW	Chitobiase; reporter gene; dnaA gene; promoter; vector; pDYK9; ds.								
XX									
OS	Escherichia coli.								
OS	Vibrio harveyi.								
OS	Chimeric.								
XX									
PN	WC200127322-A2.								
XX									
FD	19-APR-2001.								
XX									
PF	02-AUG-2000; 2000WC-US021048.								
XX									
PR	13-OCT-1999; 99US-0159221P.								
XX									
PA	(ELIT-) ELITRA PHARM INC.								
XX									
PI	Zyskind J;								
XX									
DR	WPI; 2001-290731/30.								
XX									
PT	Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.								
XX									
PS	Example 1; Page 29-30; 44pp; English.								
XX									
CC	The present sequence is that of vector plasmid pDYK9, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia coli dnaA promoter in plasmid PACYC184. pDYK9 was used to assess the regulation of the dnaA gene using chitobiase as a reporter enzyme. A claimed reporter gene construct comprises pDYK9. The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; CC detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene system in that it is not necessary to engineer many host								

CC	cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise
CC	OS field)
XX	
SQ	Sequence 5826 BP; 1574 A; 1346 C; 1389 G; 1517 T; 0 U; 0 Other;
	Query Match 100.0%; Score 243; DB 4; Length 5826;
	Best Local Similarity 100.0%; Freq. No. 1.9e-40;
	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TCTGTTACAGTCACTAATACCATCTAAAGTAGTTGATTTCATAGTGACTGCATATGTTGTG 60
Dd	4888 TCTGTTACAGTCACTAATACCATCTAAGTAGTTGATTTCATAGTGACTGCATATGTTGTG 4947
QY	61 TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATATTTTA 120
Dd	4948 TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATATTTTA 5007
QY	121 TAATCATTTTACGGTTCCTCGTTCAGCTTTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 180
Dd	5008 TATCATTTTACGGTTCCTCGTTCAGCTTTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 5067
QY	181 GCATTATCAAATTGTTGCCAAGAACAGCTCACTATCAGTCAAAATATAAATCATTTATTGAT 240
Dd	5068 GCATTATCAAATTGTTGCCAAGAACAGCTCACTATCAGTCAAAATATAAATCATTTATTGAT 5127
QY	241 TTC 243
Dd	5128 TTC 5130
RESULT 15	
AAF30799	ID AAF30799 standard; DNA; 6071 BP.
XX	AC AAF30799;
XX	DT 11-SEP-2003 (revised)
DT	21-JUN-2001 (first entry)
XX	Vector plasmid pDYK11 encoding dnaA-chitobiase fusion.
DE	
XX	Chitobiase; reporter gene; dnaA gene; promoter; vector; pDYK11; ds.
KW	
OS	Escherichia coli.
OS	Vibrio harveyi.
OS	Chimeric.
XX	
PH	Key Location/Qualifiers
FT	CDS 2331..4973
FT	/*tag= a
FT	/product= "dnaA/chitobiase fusion"
XX	
XX	WO200127322-A2.
PN	
XX	19-APR-2001.
PD	
XX	02-AUG-2000; 2000WO-US021048.
Pf	
XX	13-OCT-1999; 99US-0159221P.
PR	
XX	(ELIT-) ELITRA PHARM INC.
PA	
XX	Zyskind J;
PI	
XX	WI; 2001-290731/30.
DR	P-PADB; AAB20485.
DR	
XX	
PT	Identifying a regulatory element capable of directing or regulating
PT	transcription (e.g. a promoter) comprises providing a construct linked to
PT	a nucleic acid encoding a cytoplasmic form of chitobiase.
XX	
PS	Example 1; Page 30-32; 44pp; English.
XX	

CC The present sequence is that of vector plasmid pDYK11, which comprises
CC the Vibrio harveyi chitinase gene under the control of the Escherichia
CC coli rpmH-dnaA promoter in plasmid pACYC184. The plasmid encodes a dnaA-
CC chitinase fusion protein (see AAB20485). It was used to assess the
CC regulation of the dnaA gene using chitinase as a reporter enzyme. A
CC claimed reporter gene construct comprises pDYK11. The invention relates
CC to genetic constructs and methods of using a cytoplasmic form of
CC chitinase enzyme as a reporter. The invention also comprises expression
CC vectors which express the cytoplasmic form of chitinase. Methods are
CC provided for: characterizing a promoter; identifying a regulatory element
CC capable of directing and regulating transcription within a test sequence;
CC detecting a successful transformation; and for monitoring the activity of
CC a promoter. Chitinase has an advantage over beta-galactosidase as a
CC reporter gene in that it is not necessary to engineer many host cells to
CC lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
XX

SQ Sequence 6071 BP; 1638 A; 1400 C; 1451 G; 1582 T; 0 U; 0 Other;
Query Match 100.0%; Score 243; DB 4; Length 6071;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCGATTCATAGTCACTGATATGTTG 60
Db 5133 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCGATTCATAGTCACTGATATGTTG 5192
QY 61 TTTTACAGTATATGATGTCCTGTTTTTATGCAAAATCTAATTTAATATATGATATTA 120
Db 5193 TTTTACAGTATATGATGTCCTGTTTTTATGCAAAATCTAATTTAATATATGATATTA 5252
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATCTAAGTTGGCATTTAAAAAGCATT 180
Db 5253 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATCTAAGTTGGCATTTAAAAAGCATT 5312
QY 181 GCTTATCAATTTGTTGCAACGAGGTCATCATGTCAGTCAAAATATAATTTATTTGAT 240
Db 5313 GCTTATCAATTTGTTGCAACGAGGTCATCATGTCAGTCAAAATATAATTTATTTGAT 5372
QY 241 TTC 243
Db 5373 TTC 5375

Search completed: September 9, 2004, 18:05:39
Job time : 277.724 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 ; Search time 1962.91 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

Sequence: 1 tctgtacagtgtaataa.....taaaatcattattgatttc 243

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	243	100.0	712	28	AQ990809
C 2	214.8	88.4	395	28	AQ991303
C 3	211.4	87.0	769	28	AQ990470
C 4	208.8	85.9	764	28	AQ990878
					Rfc01715

C 5	197	81.1	472	13	BQ157398
C 6	197	81.1	473	13	BQ156404
C 7	187.4	77.1	751	28	AQ989566
C 8	186.4	76.7	743	28	AQ990346
C 9	185.6	76.4	299	13	BY115594
C 10	175.2	72.1	753	28	AQ990861
C 11	165.8	68.2	746	28	AQ990173
C 12	160.8	66.2	770	28	AQ991774
C 13	160.8	66.2	791	28	AQ991791
C 14	159.4	65.6	695	28	AQ991039
C 15	159	65.4	719	28	AQ991352
C 16	157.2	64.7	707	28	AQ990301
C 17	156.2	64.3	708	28	AQ990869
C 18	155.4	64.0	827	14	CF347641
C 19	152.8	62.9	755	14	CF347718
C 20	150.2	61.8	787	14	CF347604
C 21	150	61.7	597	12	BI422679
C 22	149	61.3	808	28	AQ990388
C 23	144	59.3	206	13	BQ156416
C 24	140	57.6	777	14	CF347686
C 25	139.6	57.4	756	28	AQ991732
C 26	135.2	55.6	715	28	AQ991358
C 27	134.6	55.4	583	14	CB403882
C 28	132.4	54.5	764	28	AQ990110
C 29	129.8	53.4	393	14	CB403984
C 30	128	52.7	664	28	AQ991011
C 31	123.6	50.9	487	14	CB395230
C 32	122.2	50.3	675	28	AQ991241
C 33	121	49.8	556	28	AQ991338
C 34	114.2	47.0	758	28	AQ991690
C 35	107	44.0	672	28	AQ990864
C 36	102.8	42.3	553	14	CF347596
C 37	100.4	41.3	360	9	AU244794
C 38	100.4	41.3	417	12	BM134283
C 39	92.4	38.0	262	14	CB395877
C 40	92.2	37.9	811	14	CF347776
C 41	91.6	37.7	622	10	BE45088
C 42	90.8	37.4	227	14	CB398923
C 43	90.8	37.4	263	14	CB395890
C 44	90.6	37.3	247	14	CB401020
C 45	89.6	36.9	381	13	BX508371

ALIGNMENTS

RESULT 1
AQ990809/c

LOCUS

DEFINITION Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG01638, genomic survey
sequence.

ACCESSION

VERSION AQ990809.1 GI:9649403

KEYWORDS

SOURCE

ORGANISM

Photobacterium luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photobacterium.

1 (bases 1 to 712)

french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,

Daborn,P.J., Bowen,D. and Biatther,F.R.

A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: french-Constant RH

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University of Bath

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Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward

Class: shotgun.

FEATURES

Location/Qualifiers
 1. .712
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 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01638"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.6e-36;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGCATCATGTTGTG 60
 Db 591 TCTGTTACAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGCATCATGTTGTG 532

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 120
 Db 531 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATTTA 472

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATPACTAAGTGGCATATATAAAACAT 180
 Db 471 TATCAATTTACGTTCTCGTTCAGCTTTTATPACTAAGTGGCATATATAAAACAT 412

QY 181 GCTATCAATTTGTTCAACAGACAGTCATCATCTCAATCAATTAATCAATTTGAT 240
 Db 411 GCTATCAATTTGTTCAACAGACAGTCATCATCTCAATCAATTAATCAATTTGAT 352

QY 241 TTC 243
 ||||
 Db 351 TTC 349

RESULT 2

AQ991303/c
 LOCUS 395 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rfc02205 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02205, genomic survey sequence.

ACCESSION AQ991303
 VERSION AQ991303.1 GI:9649897
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 395)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633
 PUBMED 10919786

COMMENT Contact: ffrench-Constant RH
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 Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward

Class: shotgun.

FEATURES

Location/Qualifiers
 1. .395
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
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 /dev_stage="primary phase variant"
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ORIGIN

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 Best Local Similarity 94.2%; Pred. No. 6.1e-31;
 Matches 227; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 3 TGTTCAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGCATCATGTTGTGTT 62
 Db 345 TGTTCAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGCATCATGTTGTGTT 287

QY 63 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATTTATA 122
 Db 286 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATTTATA 227

QY 123 TCATTTTACGTTCTCGTTCAGCTTTTATATACTAGTTGGCATTTATAAAAGCATTC 182
 Db 226 TCATTTTACGTTCTCGTTCAGCTTTTATATACTAGTTGGCATTTATAAAAGCATTC 167

QY 183 TTATCAATTTGTTGCAACGACAGTCATCATCAGTCAAAATAAAATCATTATTGATTT 242
 Db 166 TTATCAATTTGTTGCAACGACAGTCATCATCAGTCAAAATAAAATCATTATTGATTT 107

QY 243 C 243
 ||||
 Db 106 C 106

RESULT 3

AQ990470/c
 LOCUS 769 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rfc01245 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01245, genomic survey sequence.

ACCESSION AQ990470
 VERSION AQ990470.1 GI:9649064
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 769)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633
 PUBMED 10919786

COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward
Class: shotgun.

FEATURES
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1. .769
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01245"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 87.0%; Score 211.4; DB 28; Length 769;
Best Local Similarity 94.2%; Pred. No. 2.1e-30;
Matches 229; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 2 CTGTTCAGGTCACATAACATCTAAGTAGTTCATTTCATAGTGCATGCTGTTGTTGTT 61
Db 769 CTGTTCAGGTCACATCCCATTTAAAGTAGTTCATTTCATAGTGCATGCTGTTGTTGTT 710
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Db 709 TTNACAGTATATAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTAT 650
QY 122 ATCAATTTAGTTTC-TGTTACGCTTTTATTAAGTGGCATTAATAAAGCAATT 180
Db 649 ATCAATTTAGTTTC-TGTTACGCTTTTATTAAGTGGCATTAATAAAGCAATT 590
QY 181 GCTTATCAATTTGTTGCAAGACAGTCATCTATCAGTCAAAATAAATCATATTGAT 240
Db 589 GCTTATCAATTTGTTGCAAGACAGTCATCTATCAGTCAAAATAAATCATATTGAT 530
QY 241 TTC 243
Db 529 TTC 527

RESULT 4
AQ990878/c
LOCUS
DEFINITION Rfc01715 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01715, genomic survey sequence.
ACCESSION AQ990878
VERSION AQ990878.1 GI:9649472
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 764)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward
Class: shotgun.

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Location/Qualifiers
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/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 85.9%; Score 208.8; DB 28; Length 764;
Best Local Similarity 97.5%; Pred. No. 6.5e-30;
Matches 232; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 6 TACAGGTCACATAACATCTAAGTAGTTCATTTCATAGTGCATGCTGTTGTTT 65
Db 763 TACAGGTCACATAAACCATTAAAGTAGTTCATTTCATAGTGCATGCTGTTGTTT 704
QY 66 CAGTATTATGTCGTCGTTTATGCAAAATCTAAATTAATATATGATATTATATCA 125
Db 703 CAGTATTATGTCGTCGTTTATGCAAAATCTAAATTAATATATGATATTATCA 645
QY 126 TTTTACGTTTCTCGTTCAGCTTTTATACCTAGTGCATTAATAAAGCAATTGCTTA 185
Db 644 TTTTACGTTTCTCGTTCAG-TTTTTATACCTAGTGCATTAATAAAGCAATTGCTTA 586
QY 186 TCAATTTGTTGCAAGACAGTCATCTATCAGTCAAAATAAATCATATTGATTC 243
Db 585 TCAATTTGTTGCAAGACAGTCATCTATCAGTCAAAATAAATCATATTGATTC 528

RESULT 5
BQ157398/c
LOCUS
DEFINITION BQ157398 472 bp mRNA linear EST 24-APR-2002
NF104D07IR 5', mRNA sequence.
ACCESSION BQ157398
VERSION BQ157398.1 GI:20294457
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 472)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
JOURNAL Unpublished (2001)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 472 Std Error: 0.00
Plate: 104 row: D column: 07
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers

source

1. .472

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/dev_stage="seedling"
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/notes="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using EXAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

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ORIGIN

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Query Match      81.1%; Score 197; DB 13; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	47	CTGCATATGTTGTGTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAA	106
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Qy	107	TATATTGATATTATATCATTTTACGTTTCGTTTCAGCTTTTTTATACTAAGTTCGCAT	166
Db	412	TATATTGATATTATATCATTTTACGTTTCGTTTCAGCTTTTTTATACTAAGTTCGCAT	353
Qy	167	TATAAAAAGCATTCCTTATCAAATTGTTGCAACGAACAGGTCACTATCAAGTCAAAATAA	226
Db	352	TATAAAAAGCATTCCTTATCAAATTGTTGCAACGAACAGGTCACTATCAAGTCAAAATAA	293
Qy	227	AATCATTAATTTGATTTC	243
Db	292	AATCATTAATTTGATTTC	276

RESULT 6

BQ156404/c					
LOCUS	BQ156404	473 bp	mRNA	linear	EST 24-APR-2002
DEFINITION	NF092E03IRIF1023	Irradiated	Medicago truncatula	cDNA clone	
	NF092E03IR 5'		mRNA sequence.		

Accession
BQ156404
Version
BQ156404.1
Keywords
GT:20293463
Source
Medicago truncatula (barrel medic)
Organism
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 473)
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Imman, J.T., Wellner, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula irradiated library

JOURNAL COMMENT

Unpublished (2001)

Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 473 Std Error: 0.00

FEATURES
SOU

Plate: 092 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.

Location/Qualifiers
1. .473

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/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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/tissue_type="seedlings"
/dev_stage="seedling"
/clone_lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using Exassit
helper phage and the E. coli strain Xli-Blue MRF+
(Stratagene). Excised plasmids were plated using SOIR
cells."

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ORIGIN

	Query Match	81.1%;	Score 197;	DB 13;	Length 473;
	Best Local Similarity	100.0%;	Pred. No. 1.3e-27;		
	Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	47	CTGCATATGTTGGTTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAA	106		
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Qy	107	TATATTGATATTATATATCATTTTTTACGTTTCTCGTTTTCGTTTTTTATCTAAAGTTGGCAT	166		
Db	413	TATATTGATATTATATATCATTTTTTACGTTTCTCGTTTTCGTTTTTTATCTAAAGTTGGCAT	354		
Qy	167	TATAAAAAGCATTGCTTTATCAATTGTTGGCAACGACAGTCACTATCATGTCAAAATAA	226		
Db	353	TATAAAAAGCATTGCTTTATCAATTGTTGGCAACGACAGTCACTATCATGTCAAAATAA	294		
Qy	227	AATCATTATTGATTTC	243		
Db	293	AATCATTATTGATTTC	277		

DECIII.T 7

Accession	AF098956	751 bp	DNA	linear	GSS 14-AUG-2000
LOCUS	RF00126	Photorhabdus luminescens strain w14 M13 library			
DEFINITION	Photorhabdus luminescens genomic clone PLG00126, genomic survey sequence.				
VERSION	AQ089566				
KEYWORDS	AQ089566.1	GI:9648160			
SOURCE	GSS.				
ORGANISM	Photorhabdus luminescens				
	Photorhabdus luminescens				
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.				
REFERENCE	1' (bases 1 to 751)				
AUTHORS	French-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.				
TITLE	A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens w14: potential implications for virulence				
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)				
MEDLINE	20378633				
PubMed	10919786				
COMMENT	Contact: french-constant RH				
	Department of Biology and Biochemistry				
	University of Bath				
	South Building, Bath BA2 7AY, UK				

Tel:	(44) 1225 826621
Fax:	(44) 1225 826779
Email:	bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.	
Seq primer:	M13 Forward
Class:	shotgun.
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	/clone_lib="Photorhabdus luminescens strain W14 M13 library"
	/note="genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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Best Local Similarity	95.5%; Pred.No. 6,7e-26;
Matches 213; Conservative 0; Mismatches -8; Indels 2; Gaps 2	
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QY	749 CCCAATTAGAGTGCATTCATAG-CACTGCATATGTTGGTTTACAG-ATAATGTAGTC 692
Db	
QY	81 TGTTTTTTAAGCAAAATCTAAATTAATATATATGATATATATATCATTTACGTTTCGTCGT 140
Db	
QY	691 TGTTTTTTATGCAAAATCTAAATTAATATATATGATATATANATCATTTACGTTTCGTCGT 632
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QY	141 TCAGCTTTTTTATACTAAGTTGGCATTATATAAAGCAATCGCTTATCAATTTGTTGCAAC 200
Db	
QY	631 TCAGCTTTTTTATANTAAGTTGGCATTATATAAAGCAATCGCTTATCAATTTGTTGCAAC 572
Db	
QY	201 GAACAGCTCACTATCAGTCAAATAAAATCATTTATTCGATTTC 243
Db	
QY	571 GAACAGCTCACTATCAGTCAAATAAAATCATTTATTCGATTTC 529
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RESULT 8	
AQ990346/c	743 bp DNA linear GSS 14-AUG-2000
LOCUS	Rfc01106 Photorhabdus luminescens strain W14 M13 library
DEFINITION	Photorhabdus luminescens genomic clone PLG01106, genomic survey sequence.
ACCESSION	AQ990346.1 GI:9648940
VERSION	AQ990346
KEYWORDS	GSS.
SOURCE	Photorhabdus luminescens
ORGANISM	Photorhabdus luminescens
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
AUTHORS	1 (bases 1 to 743) french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blatner,F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL	20378633
MEDLINE	1091986
PUBMED	Contact: french-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK
COMMENT	Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bssrfc@bath.ac.uk This is one of 2,122 random reads from the M13 library. For

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yangtsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakayama, N., Sato, K., Shiraki, T., Waki, K., Wajai, J., Aizawa, K., Akawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Laufer, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature	420, 563-573 (2002)
JOURNAL OF MEDICAL GENETICS	22354683
INDEXED FOR MEDLINE	12466851
INDEXED FOR PUBMED	

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp
 URL: <http://genome.sgc.riken.go.jp/>
 Aizawa, K., Akimura, T., Arakawa, I., Carninci, P., Fukuda, S.,
 Hayashizaki, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

10 (11), 1757-1771 (2000).
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES	SOURCE
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Location/Qualifiers
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Db 108 TCTGTCACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGG 167

Qy 61 TTTTACAGTATTAAGTAGTCTGTTTTTTTATGCAAAATCTAAATTAATAATTGATATTTA 120

Db 168 TTTCACAGTATTAAGTAGTCTGTTTTTTTATGCAAAATCTAAATTAATAATTGATATTTA 227

Qy	121	TATCA	TTTTACG	TTTCTCG	TTTTCAC	TTTTTAT	ACTAAG	TTGGCA	TATAAAAAG	CATT	180
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Qy	181	GCTTATCAATT	192
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LOCUS	RFC01698	Photorhabdus luminescens strain W14 M13 library	
DEFINITION	Photorhabdus luminescens genomic clone PLG01698, genomic survey sequence.		
ACCESSION	AQ990861		
VERSION	AQ990861.1	GI:9649455	
KEYWORDS	GSS.		
SOURCE	Photorhabdus luminescens		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.		
REFERENCE	1 (bases 1 to 753)		
AUTHORS	ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.		
TITLE	A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens w14: potential implications for virulence		
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)		
MEDLINE	20378633		
PUBMED	10919786		
COMMENT	Contact: ffrench-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel.: (44) 1225 826621 Fax: (44) 1225 826779 Email: bssrfc@bath.ac.uk This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Forward Class: Shotgun.		
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	Best Local Similarity	95.5%;	Pred. No. 1.3e-23;
	Matches 210; Conservative	0; Mismatches	7; Indels 3; Gaps 3;
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Qy	84	TTTTTATGCCAAATCTAATTATATATATTCATATTATATCATTTTACGTTTCCTCGTCA	143
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Qy	144	GCITTTTTTACTAAGTTGGCATTATATAAAAAAGCATTGGCTTATCAATTTGTTGCAACGAA	203
Dd	633	GCITTTTTTACTAAG-TGSCATTATATAAAAAGCATTGCTTATCAATTTGTTGCAACGAA	575
Qy	204	CAGTCACTATCAGTCAAATAAAATCATTTATTGATTTC	243
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RESULT 11
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LOCUS
DEFINITION
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RfC00898 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00898, genomic survey
sequence.

ACCESSION
AQ990173
VERSION
AQ990173.1 GI:9648767
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 746)
AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

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library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

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Best Local Similarity 97.4%; Pred. No. 7.5e-22;
Matches 189; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 51 ATATGTTGCTTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATA 110
Db 723 ATATGTTGCTTTTACAG-ATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATA 665
QY 111 TTGATATTTATATCATTTTACGTTCTCGTTCAGCTTTTTTATACCTAAGTTGGCAATTATA 170
Db 664 TTGATATTTANATCATTTTACGTTCTCGTTCAGTTTTTTATATTAAGTTGGCAATTATA 605
QY 171 AAAAGCAATTGCTTATCAA-TTTGTTCCAGCAACAGGTCAGTCTATCATGTCAAAATAAAT 229
Db 604 AAAAGCAATTGCTTATCAA-TTTGTTCCAGCAACAGGTCAGTCTATCATGTCAAAATAAAT 545
QY 230 CATTAATTGATTTC 243
Db 544 CATTAATTGATTTC 531

RESULT 12
AQ991774/c
LOCUS
DEFINITION
770 bp DNA linear GSS 14-AUG-2000
RfC02039F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02039F, genomic survey
sequence.

ACCESSION
AQ991774
VERSION
AQ991774.1 GI:9650368
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 770)
AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.

FEATURES
source
1..770
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02039F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 66.2%; Score 160.8; DB 28; Length 770;
Best Local Similarity 98.8%; Pred. No. 6.4e-21;
Matches 162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGATGTTGTG 60
Db 197 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGATGTTGTG 138
QY 61 TTTTACAGATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATTCATATTTA 120
Db 137 TTTTACAGATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATTCATATTTA 78
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACCTAAGTTGGC 164
Db 77 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACCTAAGTTGAC 34

RESULT 13
AQ991791/c
LOCUS
DEFINITION
791 bp DNA linear GSS 14-AUG-2000
RfC02368F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02368F, genomic survey
sequence.

ACCESSION
AQ991791
VERSION
AQ991791.1 GI:9650385
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens

ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 791)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
JOURNAL Photorhabdus luminescens W14: potential implications for virulence
MEDLINE Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 20378633
COMMENT 10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (SLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.

FEATURES
source 1..791
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02368F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 66.2%; Score 160.8; DB 28; Length 791;
Best Local Similarity 98.8%; Pred. No. 6.4e-21;
Matches 162; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTCATGCGATGTTCTG 60
Db 194 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTCATGCGATGTTCTG 135

QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAGAACTAATTAAATATATGATATTATTA 120
Db 134 TTTTACAGTATTATGTAGTCTGTTTTTATGCAGAACTAATTAAATATATGATATTATTA 75

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATATACTAAGTTGGC 164
Db 74 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATATACTAAGTTGAC 31

RESULT 14
AQ991039/c
LOCUS
DEFINITION
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens strain W14 M13 library
sequence.

ACCESSION AQ991039
VERSION AQ991039.1
KEYWORDS GI:9649633
SOURCE GSS.
ORGANISM Photorhabdus luminescens
Photobacterium luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 695)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence

Search completed: September 9, 2004, 21:18:23
Job time : 1964.91 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 306.981 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

Sequence: 1 tcgttacaggtcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	100.0	243	13	US-10-403-232-173
2	243	100.0	243	17	US-10-310-695-14
3	243	100.0	248	17	US-10-627-711-8
4	243	100.0	282	15	US-10-161-403-72
C 5	243	100.0	1763	11	US-09-244-805-57
C 6	243	100.0	1763	11	US-09-245-277-57
7	243	100.0	1763	17	US-10-792-481-57
8	243	100.0	4346	15	US-10-161-403-113
9	238.2	98.0	243	17	US-10-310-695-2
10	231	95.1	2959	13	US-10-270-176-8
11	231	95.1	3663	13	US-10-270-176-3
12	231	95.1	3695	13	US-10-270-176-13
13	231	95.1	4782	13	US-10-270-176-20
14	231	95.1	5646	13	US-10-270-176-41

15	231	95.1	5706	13	US-10-270-176-40	Sequence 40, Appl
16	231	95.1	5739	13	US-10-270-176-9	Sequence 9, Appl
17	231	95.1	5771	13	US-10-270-176-34	Sequence 34, Appl
18	231	95.1	5771	13	US-10-270-176-35	Sequence 35, Appl
19	231	95.1	5814	13	US-10-270-176-37	Sequence 37, Appl
20	231	95.1	5911	13	US-10-270-176-42	Sequence 42, Appl
21	231	95.1	5929	13	US-10-270-176-45	Sequence 45, Appl
22	231	95.1	5929	13	US-10-270-176-46	Sequence 46, Appl
23	231	95.1	5948	13	US-10-270-176-21	Sequence 21, Appl
24	231	95.1	5986	13	US-10-270-176-36	Sequence 36, Appl
25	231	95.1	6200	13	US-10-270-176-38	Sequence 38, Appl
26	231	95.1	6664	13	US-10-270-176-1	Sequence 1, Appl
27	231	95.1	6668	13	US-10-270-176-2	Sequence 2, Appl
28	231	95.1	6742	13	US-10-270-176-19	Sequence 19, Appl
C 29	226.8	93.3	4470	15	US-10-151-690-21	Sequence 21, Appl
C 30	226.8	93.3	4892	16	US-10-357-268-1	Sequence 1, Appl
31	226.8	93.3	5584	15	US-10-151-690-61	Sequence 61, Appl
32	226.8	93.3	17862	15	US-10-055-001A-23	Sequence 23, Appl
C 33	226.8	93.3	17862	15	US-10-055-001A-23	Sequence 23, Appl
34	226.8	93.3	18691	15	US-10-055-001A-13	Sequence 13, Appl
C 35	226.8	93.3	18691	15	US-10-055-001A-13	Sequence 13, Appl
36	226.6	93.3	233	13	US-10-301-849A-16	Sequence 16, Appl
C 37	226.6	93.3	233	13	US-10-403-232-177	Sequence 177, App
38	225.4	92.8	4428	15	US-10-151-690-62	Sequence 62, Appl
39	225.4	92.8	4470	15	US-10-151-690-21	Sequence 21, Appl
40	225.4	92.8	4627	15	US-10-151-690-63	Sequence 63, Appl
41	225.4	92.8	4627	15	US-10-151-690-64	Sequence 64, Appl
42	225.4	92.8	4892	16	US-10-357-268-1	Sequence 1, Appl
C 43	225.4	92.8	5584	15	US-10-151-690-61	Sequence 61, Appl
44	225	92.6	233	13	US-10-403-232-179	Sequence 179, App
C 45	220.4	90.7	4428	15	US-10-151-690-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-403-232-173
; Sequence 173, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Gludeng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403.232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-173

Query Match	100.0%;	Score 243;	DB 13;	Length 243;
Best Local Similarity	100.0%;	Pred. No. 1e-40;		
Matches 243;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TCGTTCACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGATGTTGTG	60	
Db	1	TCGTTCACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGATGTTGTG	60	
Qy	61	TTTTCACAGTATTAGTACTGTGTTTTTATGCAAAATCTAATTATATATATGATTTA	120	
Db	61	TTTTCACAGTATTAGTACTGTGTTTTTATGCAAAATCTAATTATATATATGATTTA	120	
Qy	121	TATCATTTTACGTTCTCGTTTCAGCTTTTTTATACAAAGTTGGCATTATAAAAGCATT	180	
Db	121	TATCATTTTACGTTCTCGTTTCAGCTTTTTTATACAAAGTTGGCATTATAAAAGCATT	180	

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QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
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Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
      |||||||
QY 241 TTC 243
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Db 241 TTC 243
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RESULT 2
US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:019JS
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

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Query Match 100.0%; Score 243; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 60
Db 1 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 60
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QY 61 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 120
Db 61 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 120
      |||||||
QY 121 TATCATTATACGTTTCTCGTTCAGCTTTTATPACTAAGTTGGCAATATAAAAAAGCAAT 180
Db 121 TATCATTATACGTTTCTCGTTCAGCTTTTATPACTAAGTTGGCAATATAAAAAAGCAAT 180
      |||||||
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
      |||||||
QY 241 TTC 243
      |||
Db 241 TTC 243
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RESULT 3
US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; SCREENING OF CDNA CLONES
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:

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; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 100.0%; Score 243; DB 17; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 60
Db 1 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 60
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QY 61 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 120
Db 61 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 120
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QY 121 TATCATTATACGTTTCTCGTTCAGCTTTTATPACTAAGTTGGCAATATAAAAAAGCAAT 180
Db 121 TATCATTATACGTTTCTCGTTCAGCTTTTATPACTAAGTTGGCAATATAAAAAAGCAAT 180
      |||||||
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
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QY 241 TTC 243
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Db 241 TTC 248
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RESULT 4
US-10-161-403-72
; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp
US-10-161-403-72

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Query Match 100.0%; Score 243; DB 15; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 60
Db 15 TCTGTTACAGGTCACATTAACCATTAAGTAGTGTGATTCATAGTGAAGTGTG 74
      |||||||
QY 61 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 120
Db 75 TTTTACAGTATTATGATGCTGCTGTTTATGCAAAATCTAAATTAATATATTGATTTA 134
      |||||||
QY 121 TATCATTATACGTTTCTCGTTCAGCTTTTATPACTAAGTTGGCAATATAAAAAAGCAAT 180
      |||||||

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Db      135 TATCATTTTACGTTCTTCGTTGAGCTTTTATATACTAGTTGGCATTATATAAAAGCAAT 194
QY      181 GCTTATCAATTTGTTGCAAGAACAGTCTACATATAGTCAAAATAAATCAATATTGAT 240
Db      195 GCTTATCAATTTGTTGCAAGAACAGTCTACATATAGTCAAAATAAATCAATATTGAT 254
QY      241 TTC 243
Db      255 TTC 257

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RESULT 5

US-09-244-805-57/c
 ; Sequence 57, Application US/09244805
 ; Publication No. US20030203840A1

; GENERAL INFORMATION:
 ; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony
 ; APPLICANT: Goetz, Bernard

; APPLICANT: Heimisch, Holger
 ; APPLICANT: Kuner, Rohini

; APPLICANT: Scheek, Sigrid
 ; APPLICANT: Nikolich, Karoly

; APPLICANT: Zhukovski, Eugene
 ; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 10496/004001

; CURRENT APPLICATION NUMBER: US/09/244,805
 ; EARLIER FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: 60/074,518
 ; EARLIER FILING DATE: 1998-02-12

; EARLIER APPLICATION NUMBER: 60/074,135
 ; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 57
 ; LENGTH: 1763

; TYPE: DNA
 ; ORGANISM: Eukaryote

; FEATURE:
 ; NAME/KEY: misc_feature

; LOCATION: (1)...(1763)
 ; OTHER INFORMATION: Y = C or T

; OTHER INFORMATION: n = A,T,C or G
 US-09-244-805-57

Query Match 100.0%; Score 243; DB 11; Length 1763;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTCACTGCTGATATGTTGTG 60
Db      431 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTCACTGCTGATATGTTGTG 372
QY      61 TTTTACAGTATTATGATGTCGTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db      371 TTTTACAGTATTATGATGTCGTTTATGCAAAATCTAATTAATATATTGATATTTA 312
QY      121 TATCATTTTACGTTTCTCGTTACGTTTATGCAAAATCTAATTAATATATTGATATTTA 180
Db      311 TATCATTTTACGTTTCTCGTTACGTTTATGCAAAATCTAATTAATATATTGATATTTA 252
QY      181 GCTTATCAATTTGTTGCAAGAACAGTCTATCAGTCAAAATAAATCAATATTGAT 240
Db      251 GCTTATCAATTTGTTGCAAGAACAGTCTATCAGTCAAAATAAATCAATATTGAT 192
QY      241 TTC 243
Db      191 TTC 189

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RESULT 6

US-09-245-277-57/c

; Sequence 57, Application US/09245277
 ; Publication No. US20030211984A1

; GENERAL INFORMATION:
 ; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony
 ; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: JHU1530-3

; CURRENT APPLICATION NUMBER: US/09/245,277
 ; CURRENT FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 60/074,518
 ; PRIOR FILING DATE: 1998-02-12

; PRIOR APPLICATION NUMBER: 60/074,135
 ; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 57
 ; LENGTH: 1763

; TYPE: DNA
 ; ORGANISM: Eukaryote

; FEATURE:
 ; NAME/KEY: misc_feature

; LOCATION: (1)...(1763)
 ; OTHER INFORMATION: Y = C or T

; OTHER INFORMATION: n = A,T,C or G
 US-09-245-277-57

Query Match 100.0%; Score 243; DB 11; Length 1763;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTCACTGCTGATATGTTGTG 60
Db      431 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTCACTGCTGATATGTTGTG 372
QY      61 TTTTACAGTATTATGATGTCGTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db      371 TTTTACAGTATTATGATGTCGTTTATGCAAAATCTAATTAATATATTGATATTTA 312
QY      121 TATCATTTTACGTTTCTCGTTACGTTTATGCAAAATCTAATTAATATATTGATATTTA 180
Db      311 TATCATTTTACGTTTCTCGTTACGTTTATGCAAAATCTAATTAATATATTGATATTTA 252
QY      181 GCTTATCAATTTGTTGCAAGAACAGTCTATCAGTCAAAATAAATCAATATTGAT 240
Db      251 GCTTATCAATTTGTTGCAAGAACAGTCTATCAGTCAAAATAAATCAATATTGAT 192
QY      241 TTC 243
Db      191 TTC 189

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RESULT 7

US-10-792-481-57/c

; Sequence 57, Application US/10792481
 ; Publication No. US20040152658A1

; GENERAL INFORMATION:
 ; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony
 ; APPLICANT: Goetz, Bernard

; APPLICANT: Heimisch, Holger
 ; APPLICANT: Kuner, Rohini

; APPLICANT: Scheek, Sigrid
 ; APPLICANT: Nikolich, Karoly

; APPLICANT: Zhukovski, Eugene
 ; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 10496/004001

; CURRENT APPLICATION NUMBER: US/10/792,481
 ; CURRENT FILING DATE: 2004-03-02

; PRIOR APPLICATION NUMBER: US/09/244,805
 ; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 60/074,518

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; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-10-792-481-57

Query Match
Best Local Similarity 100.0%; Score 243; DB 17; Length 1763;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTGACTGCATATGTTGTG 60
Db 431 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTGACTGCATATGTTGTG 372

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 371 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 312

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 180
Db 311 TATCATTTTACGTTTCTCGTTCAGCTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 252

QY 181 GCTTATCAATTTGTTGCAAGACAGGTCACCTATCAGTCAAAATATAAAATCATTATTGAT 240
Db 251 GCTTATCAATTTGTTGCAAGACAGGTCACCTATCAGTCAAAATATAAAATCATTATTGAT 192

QY 241 TTC 243
Db 191 TTC 189

RESULT 8
US-10-161-403-113
; Sequence 113, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 4346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSV40-193AttppensePur Plasmid
US-10-161-403-113

Query Match
100.0%; Score 243; DB 15; Length 4346;

Query Match
Best Local Similarity 98.0%; Score 238.2; DB 17; Length 243;
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTGACTGCATATGTTGTG 60
Db 1 TCTGTTACAGGTCACCTAATACCACTAAGTAGTGTGATTCATAGTGACTGCATATGTTGTG 60

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 180
Db 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACCTAAGTTGGCATTATAAAAAAGCATT 180

QY 181 GCTTATCAATTTGTTGCAAGACAGGTCACCTATCAGTCAAAATATAAAATCATTATTGAT 240
Db 181 GCTTATCAATTTGTTGCAAGACAGGTCACCTATCAGTCAAAATATAAAATCATTATTGAT 240

QY 241 TTC 243
Db 241 TTC 243

RESULT 10
US-10-270-176-8
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; Sequence 8, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2959
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-8

Query Match      95.1%; Score 231; DB 13; Length 2959;
Best Local Similarity 99.2%; Pred. No. 6.6e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGC--ATATGTTG 58
Db 939 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGCATATATGTTG 998

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 118
Db 999 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 1058

QY 119 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 178
Db 1059 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 1118

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 238
Db 1119 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 1178

QY 239 ATTTC 243
Db 1179 ATTTC 1183

RESULT 11
US-10-270-176-3
; Sequence 3, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-3

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Query Match      95.1%; Score 231; DB 13; Length 3663;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGC--ATATGTTG 58
Db 1643 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGCATATATGTTG 1702

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 118
Db 1703 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 1762

QY 119 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 178
Db 1763 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 1822

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 238
Db 1823 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 1882

QY 239 ATTTC 243
Db 1883 ATTTC 1887

RESULT 12
US-10-270-176-13
; Sequence 13, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 3695
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-13

Query Match      95.1%; Score 231; DB 13; Length 3695;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGC--ATATGTTG 58
Db 1675 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTACTGCATATATGTTG 1734

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 118
Db 1735 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATT 1794

QY 119 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 178
Db 1795 TATATCATTTTACGTTTCCTGTTTCAGCTTTTATACCTAAGTTGGCAATATAAAAAAGCA 1854

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 238
Db 1855 TTGCTTATCAATTTGTTGCAACGACAGTCACCTATCAGTCAAAATCAATTCATTTT 1914

QY 239 ATTTC 243
Db 1915 ATTTC 1919

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FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-41

Query Match      95.1%; Score 231; DB 13; Length 5646;
Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 3968 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 4027

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 4028 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 4087

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 178
Db 4088 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 4147

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 238
Db 4148 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 4207

QY 239 ATTTC 243
Db 4208 ATTTC 4212

RESULT 15
US-10-270-176-40
; Sequence 40, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 40
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-40

Query Match      95.1%; Score 231; DB 13; Length 5706;
Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 3968 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 4027

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 4028 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 4087

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 178
Db 4088 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 4147

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 238
Db 4148 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 4207
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US-10-270-176-20
; Sequence 20, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 20
; LENGTH: 4782
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-20

Query Match      95.1%; Score 231; DB 13; Length 4782;
Best Local Similarity 99.2%; Pred. No. 7.7e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 2688 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 2747

QY 59 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 2748 TGTGTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 2807

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 178
Db 2808 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACTAAGTTGGCAATTAATAAAGCA 2867

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 238
Db 2868 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAAATCATTTATTG 2927

QY 239 ATTTC 243
Db 2928 ATTTC 2932

RESULT 14
US-10-270-176-41
; Sequence 41, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 41
; LENGTH: 5646
; TYPE: DNA
; ORGANISM: artificial
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QY 239 ATTIC 243
|||
Db 4208 ATTIC 4212

Search completed: September 10, 2004, 00:14:07
Job time : 307.981 secs

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GenCore version 5.1.6
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35: em_htg_rod.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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4	102	100.0	1421	10	AF1212976	AF1212976 Mus muscu
5	102	100.0	2408	6	AR059581	AR059581 Sequence
6	102	100.0	2408	6	AR063063	AR063063 Sequence
7	102	100.0	2408	6	I93548	I93548 Sequence 69
8	102	100.0	2408	6	AR370418	AR370418 Sequence
9	102	100.0	3049	6	AX430197	AX430197 Sequence
10	102	100.0	3049	6	AX449167	AX449167 Sequence
11	102	100.0	3111	8	CPPERAS	X52304 Chlamydomon
12	102	100.0	3484	6	A51914	A51914 Sequence 1
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14	102	100.0	3484	6	AR372694	AR372694 Sequence
15	102	100.0	3484	6	BD007602	BD007602 Nematoda-
16	102	100.0	3757	6	AR080463	AR080463 Sequence
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18	102	100.0	5349	6	A71437	A71437 Sequence 7
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25	102	100.0	9819	8	ZMA428542	AJ428542 Zea mays
26	102	100.0	9918	1	AE005255	AE005255 Escherich
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32	100.4	98.4	201	6	I36498	I36498 Sequence 18
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34	100.4	98.4	361	7	LAMINTATT	M23841 Bacterioph
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36	100.4	98.4	1668	9	NACHRS	D85521 Macaca fasc
37	100.4	98.4	1763	6	BD225932	BD225932 Immediate
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ALIGNMENTS

RESULT 1
AX092114
LOCUS AX092114 102 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 3 from Patent WO0116345.
ACCESSION AX092114
VERSION AX092114.1 GI:13444357
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
REFERENCE 1
AUTHORS Drooge,P.
TITLE Sequence-specific dna recombination in eukaryotic cells
JOURNAL Patent: WO 0116345-A 3 08-MAR-2001;
Enterobacteriaceae; Escherichia.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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    Droege, Peter (DE)
    Location/Qualifiers
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      /mol_type="unassigned DNA"
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ORIGIN
Query Match      100.0%; Score 102; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 60
Db 1 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 60

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102

RESULT 2
HUMDTN02
LOCUS      HUMDTN02      979 bp      DNA      linear      PRI 21-NOV-2001
DEFINITION Human dystrobrevin (DTN) gene, exon 2.
ACCESSION  U84530
VERSION     U84530.1 GI:2149295
KEYWORDS
SEGMENT
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 979)
AUTHORS     Sadoulet-Puccio,H.M., Feener,C.A., Schaid,D.J., Thibodeau,S.N.,
            Michels,V.V. and Kunkel,L.M.
TITLE       The genomic organization of human dystrobrevin
JOURNAL     Neurogenetics 1 (1), 37-42 (1997)
MEDLINE    20197320
PUBMED     10735273
REFERENCE   2 (bases 1 to 979)
AUTHORS     Sadoulet-Puccio,H.M., Feener,C.A. and Kunkel,L.M.
DIRECT SUBMISSION
TITLE       Submitted (09-JAN-1997) Genetics, HHMI, 320 Longwood Avenue,
            Boston, MA 02115, USA
FEATURES
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      /end=530
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ORIGIN
Query Match      100.0%; Score 102; DB 9; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 60
Db 83 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 142

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 143 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 184

RESULT 3
HSA325746/c
LOCUS      HSA325746      1090 bp      DNA      linear      PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
            NBI-850S.
ACCESSION  AJ325746
VERSION     AJ325746.1 GI:15870140
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1090)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
            Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE       NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
JOURNAL     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE    2213767
PUBMED     12136098
REFERENCE   2 (bases 1 to 1090)
AUTHORS     Zabarovsky,E.R.
DIRECT SUBMISSION
TITLE       Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES
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      /clone="NBI-850S"

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Query Match      100.0%; Score 102; DB 9; Length 1090;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 60
Db 264 CTGCTTTTATCTAAGTGGCATTTATAAAAGCAATTCCTTATCAATTTGTCGAACG 205

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 204 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 163

RESULT 4
AF121976
LOCUS      AF121976      1421 bp      DNA      linear      ROD 07-DEC-1999
DEFINITION Mus musculus odorant receptor S19 gene, complete cds.
ACCESSION  AF121976
VERSION     AF121976.2 GI:6532000
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 442 to 1421)
AUTHORS     Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
TITLE       Combinatorial receptor codes for odors
JOURNAL     Cell 96 (5), 713-723 (1999)
MEDLINE    99189756
PUBMED     10089886
REFERENCE   2 (bases 442 to 1421)
AUTHORS     Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
DIRECT SUBMISSION
TITLE       Submitted (20-JAN-1999) Neurobiology, Harvard Medical School, 220
            Longwood Avenue, Boston, MA 02115, USA
JOURNAL
REFERENCE   3 (bases 1 to 1421)
AUTHORS     Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
DIRECT SUBMISSION
TITLE       Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
            Longwood Avenue, Boston, MA 02115, USA
JOURNAL

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REMARK Sequence update by submitter
COMMENT On Dec 7, 1999 this sequence version replaced gi:4680261.

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291. .1310
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/db_xref="GI:6532001"
/translation="MPERKMLSKLIAYLLILIESCRQTAQLVKGRIWVDSRPHWNTTH
YRELDQHWTAIFPCSMYIALVNGTILYIIIDRALHEPMYFLCLLSITDLVLC
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TSILNAVVIKGLACVTGRLLFVFPVILIERLPCGHHIIPHTYCEHMGIAKLACA
SIKPNITVGLTVALSVTGMVDVYLATSYLILQAVLRPSKDAQFRAFSTCGAHICVI
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Query Match 100.0%; Score 102; DB 10; Length 1421;
Best Local Similarity 100.0%; Pred. No. 1e-14; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 129 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 188
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 189 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 230

RESULT 5

AR059581
LOCUS AR059581 2408 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 69 from patent US 5840498.
ACCESSION AR059581
VERSION AR059581.1 GI:5986031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5840498-A 69 24-NOV-1998;
FEATURES Location/Qualifiers
source 1. .2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 6

AR063063

LOCUS AR063063 2408 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 69 from patent US 5844072.
ACCESSION AR063063
VERSION AR063063.1 GI:5990754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5844072-A 69 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .2408
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 60
Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 7

AR063063
LOCUS AR063063 2408 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 69 from patent US 5731149.
ACCESSION AR063063
VERSION AR063063.1 GI:3938018
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5731149-A 69 24-MAR-1998;
FEATURES Location/Qualifiers
source 1. .2408
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/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 8

AR370418
LOCUS AR370418 2408 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 69 from patent US 6300470.
ACCESSION AR370418
VERSION AR370418.1 GI:34606949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Fri Sep 10 09:49:25 2004

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Unclassified.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 6300470-A 69 09-OCT-2001;
FEATURES Location/Qualifiers
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            /mol_type="genomic DNA"
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Query Match      100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
    |||||||
QY 61 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 102
    |||||||
Db 468 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 509
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RESULT 9
AX430197
LOCUS Beta vulgaris
DEFINITION Sequence 4 from Patent EP1207204.
ACCESSION AX430197
VERSION AX430197.1 GI:21655562
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLE Tissue-specific promoters from sugar beet
JOURNAL Patent: EP 1207204-A 4 22-MAY-2002;
KWS Saat AG (DE)
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 102; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 9e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
    |||||||
QY 61 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 102
    |||||||
Db 468 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 509
    |||||||

RESULT 9
AX430197
LOCUS Beta vulgaris
DEFINITION Sequence 4 from Patent EP1207204.
ACCESSION AX430197
VERSION AX430197.1 GI:21655562
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLE Tissue-specific promoters from sugar beet
JOURNAL Patent: EP 1207204-A 4 22-MAY-2002;
KWS Saat AG (DE)
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 102; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 9e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
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QY 61 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 102
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Db 468 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 509
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RESULT 10
AX449167
LOCUS Beta vulgaris
DEFINITION Sequence 4 from Patent WO0240687.
ACCESSION AX449167
VERSION AX449167.1 GI:21697968
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLE Tissue specific promoters
JOURNAL Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
FEATURES Location/Qualifiers
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Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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Db 2398 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 2457
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QY 61 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 102
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Db 2458 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 2499
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RESULT 10
AX449167
LOCUS Beta vulgaris
DEFINITION Sequence 4 from Patent WO0240687.
ACCESSION AX449167
VERSION AX449167.1 GI:21697968
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLE Tissue specific promoters
JOURNAL Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
FEATURES Location/Qualifiers
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QY 1 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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Db 2398 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 2457
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QY 61 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 102
    |||||||
Db 2458 AACAGTCACTATCACTCAAAATATAAATCAATTATTGATTC 2499
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RESULT 11
CRPERAS
LOCUS Chlamydomonas mRNA for periplasmic arylsulfatase.
DEFINITION Chlamydomonas mRNA for periplasmic arylsulfatase.
ACCESSION X52304
VERSION X52304.1 GI:18173
KEYWORDS arylsulfatase; AS gene; periplasmic protein.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 481 to 3111)
AUTHORS de Hostos,E.L., Schilling,J. and Grossman,A.R.
TITLE Structure and expression of the gene encoding the periplasmic
arylsulfatase of Chlamydomonas reinhardtii
JOURNAL Mol. Gen. Genet. 218 (2), 229-239 (1989)
MEDLINE 89384447
PUBMED 2476654
REFERENCE 2 (bases 1 to 3111)
AUTHORS de Hostos,E.L.
TITLE Direct Submission
JOURNAL Submitted (11-APR-1990) De Hostos E.L., Max-Planck-Institute for
Biochemistry, Am Klopferspitz 18A, 8033 Martinsried, FRG
COMMENT The sequence is a composite of a cDNA (for CDS region) and genomic.
See <X16179> for intron between bases 717-718.
See <X16180> for bases 616-3104.
FEATURES Location/Qualifiers
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            /strain="CW15."
            /db_xref="taxon:3055"
            /clone_lib="Lambda gt11 (cDNA) and EMBL4 (genomic)"
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            524..527
            /note="inverted repeat A"
            563..566
            /note="inverted repeat A'"
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/notes="unnamed protein product; protein precursor (AA -21 to 625)"
 /codon start=1
 /protein_id="CAA36545.1"
 /db_xref="GI:18174"
 /db_xref="GOA:P14217"
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 SGRWASTSPTCCQSRWTALPTTWASSLWTPPSAITSKRCGLGRYCPVTFYFDY
 NTELQNGATPNYIYGEYSTDVIRKGVAQIKSAVAAKPFYQAQISPIAPTSSTGIS
 NPATGRTSYFFPPPIVAPPHWOLFSDANIPGGSQEPLRGRERQARLDPRAAGPAE
 QHLPGGDUPFPAPELVEGVDLEIQVVKLDEAGVLDNTYIIYSADNGYHVGARFGA
 KKTGYEDLRFVFLTRPGIKASKDKPQNGKVLHVDFAPTILSLAGASHLIGDKG
 LDGTPLGLYANDDGLPSDYPRPEQHRQOFQGEFWGMSDELLQNLRSQPNNTWKVVR
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 GESCSNPWKILPDGTGNFTQALNSKIDRIYNALRPFTYKRCPLDWNDSQFKT
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 QDILKADVEKWFNFNAEYLA"
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 679..2553
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 3088..3095
 /note="polyA signal"
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 /note="polyA site"

ORIGIN

Query Match 100.0%; Score 102; DB 8; Length 3111;
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QY 1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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 Db 72 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 131
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RESULT 12

A91914
 LOCUS 3484 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 1 from Patent WO9822599.
 A91914
 ACCESSION
 A91914.1 GI:6740781
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 3484)
 OHL,S.A. and Klapp,J.
 REFERENCE
 AUTHORS OHL,S.A. and Klapp,J.
 TITLE NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
 JOURNAL Patent: WO 9822599-A 1 28-MAY-1998;
 LEE FREDERIQUE MARIANNE V D (NL); OHL STEPHAN ANDREAS (NL)

FEATURES

Location/Qualifiers
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 /protein_id="CAB69451.1"
 /db_xref="GI:6740782"
 /translation="M"

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Query Match 100.0%; Score 102; DB 6; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 8.8e-15;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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Query Match 100.0%; Score 102; DB 6; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 8.8e-15;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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 Db 420 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479
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QY 61 AACAGTCACTATCACTGCAAAATAAATCAATATTGATTTC 102
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 Db 480 AACAGTCACTATCACTGCAAAATAAATCAATATTGATTTC 521
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RESULT 13

AR309120
 LOCUS 3484 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 1 from patent US 6555529.
 AR309120
 ACCESSION
 AR309120.1 GI:31700962
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 3484)
 AUTHORS Funaba,Y., Koike,J., Tanahashi,M., Okazaki,S. and Ito,M.
 TITLE Remedies for intramedullary diseases
 JOURNAL Patent: US 6555529-A 1 29-APR-2003;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 8.8e-15;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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 Db 420 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479
 |||||

QY 61 AACAGTCACTATCACTGCAAAATAAATCAATATTGATTTC 102
 |||||
 Db 480 AACAGTCACTATCACTGCAAAATAAATCAATATTGATTTC 521
 |||||

RESULT 14

AR372694
 LOCUS 3484 bp DNA linear PAT 12-SEP-2003
 DEFINITION Sequence 1 from patent US 6395963.
 AR372694
 ACCESSION
 AR372694.1 GI:34610045
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 3484)
 AUTHORS OHL,S.A., Sijmons,P.C., Klein-Van der Lee,F.M., Goddijn,O. and
 Klapp,J.
 TITLE Nematode-inducible regulatory DNA sequences
 JOURNAL Patent: US 6395963-A 1 28-MAY-2002;
 FEATURES Location/Qualifiers
 source
 1..3484
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 8.8e-15;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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Db 420 CTGCTTTTATACATAAGTTGGCATTATATAAAAGCATTGCTTATCATCAATTGTTGCAACG 479

Qy 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTC 102
|||||
Db 480 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTC 521

RESULT 15
BD007602
LOCUS BD007602 3484 bp DNA linear PAT 31-JAN-2002
DEFINITION Nematoda-induced regulatory DNA sequence.
ACCESSION BD007602
VERSION BD007602.1 GI:18635975
KEYWORDS JP 2001503992-A/1.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 3484)
AUTHORS Andreas,S., Lee,F.M.V.D., Goddijn,O.J.M., Klap,J. and Simons,P.C.
TITLE Nematoda-induced regulatory DNA sequence
JOURNAL Patent: JP 2001503992-A 1 27-MAR-2001;
MOHEN INTERNATIONAL NV
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2001503992-A/1
PD 27-MAR-2001
PF 18-NOV-1997 JP 1998523219
PR 18-NOV-1996 EP 96203213.2
PI STEPHEN ANDREAS,FREDERIQUE MARIANNE VAN DER LEE, PI OSCAR
JOHANNES MARIA GODDIJN,JOKE KLAP,PETER CHRISTIAN SIMONS PC
C12N15/09,A01H5/00,A01N65/00,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,C12N9/22,
PC C12N15/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 3481..3484.
source Location/Qualifiers
1..3484
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 420 CTGCTTTTATACATAAGTTGGCATTATATAAAAGCATTGCTTATCATCAATTGTTGCAACG 479

Qy 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTC 102
|||||

Db 480 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTC 521

Search completed: September 9, 2004, 19:34:31
Job time : 706.078 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 : Search time 116.156 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-3

Perfect score: 102

Sequence: 1 ctgctttttataactaagt.....taaaatcattatttgatttc 102

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	102.4	100.0	102	4	Aaf61419 E. coli a
2	102	100.0	2408	2	AAT30737 Rat crypt
3	102	100.0	3049	6	Abn81284 Beet prom
4	102	100.0	3484	2	AAV34987 Arabidops
5	102	100.0	3757	2	AAV44332 Murine mm
6	102	100.0	3757	2	AAV42708 Mouse mas
7	102	100.0	5349	2	AAV23239 T-DNA of
8	102	100.0	5611	2	AAV23242 Plasmid p
9	100.4	98.4	201	2	AAQ50319 Detection
10	100.4	98.4	243	4	Aaf61418 Bacteriop
11	100.4	98.4	248	8	Acc85316 Recombina
12	100.4	98.4	282	7	Acc44676 Murine rD
13	100.4	98.4	282	7	Abt16636 Artificia
14	100.4	98.4	610	5	Aaf79770 Bacteriop
15	100.4	98.4	1469	7	Abq80306 Lambda fr
16	100.4	98.4	1469	7	Acc83020 Bacteriop
17	100.4	98.4	1763	2	Aaz30709 Rat neuro
18	100.4	98.4	4346	7	Acc44716 Plasmid p
19	100.4	98.4	4346	7	Abt16615 Artificia
20	100.4	98.4	4909	2	Aat18924 Plasmid p
21	100.4	98.4	5641	4	Aaf30800 Vector pl
22	100.4	98.4	5670	4	Aaf30801 Vector pl
23	100.4	98.4	5826	4	Aaf30798 Vector pl

ALIGNMENTS

RESULT 1

AAf61419	24	100.4	98.4	6071	4	AAf30799	Vector pl
ID AAF61419 standard; DNA; 102 BP.	25	100.4	98.4	7652	2	AAq45682	Sequencin
XX	26	98.8	96.9	243	4	AAf61421	E. coli a
AC AAF61419;	c 27	98.4	96.5	7508	8	AAI62713	Escherich
XX	c 28	93.8	92.0	100	3	AAc55386	Recombina
DT 05-JUN-2001 (first entry)	c 29	93.8	92.0	100	7	AAc55969	Nucleic a
XX	c 30	93.8	92.0	2717	3	AAc55422	Entry vec
XX	c 31	93.8	92.0	2717	3	AAc55437	Entry vec
DE E. coli attL DNA fragment.	c 32	93.8	92.0	2717	7	ABZ58764	Entry vec
XX	c 33	93.8	92.0	2718	3	AAc55425	Entry vec
Sequence-specific recombination; SSR; integrase; gene therapy; somatic;	c 34	93.8	92.0	2720	3	AAc55431	Entry vec
targeted integration; attL; ds.	c 35	93.8	92.0	2720	3	AAc55434	Entry vec
XX	c 36	93.8	92.0	2723	3	AAc55428	Entry vec
Escherichia coli.	c 37	93.8	92.0	2735	3	AAc55446	Entry vec
XX	c 38	93.8	92.0	2735	3	AAc55443	Entry vec
DEI9941186-AI.	c 39	93.8	92.0	2738	3	AAc55449	Entry vec
XX	c 40	93.8	92.0	2738	3	AAc55440	Entry vec
PD 01-MAR-2001.	c 41	93.8	92.0	2744	3	AAc55452	Entry vec
PF 30-AUG-1999; 99DE-01041186.	c 42	92.2	90.4	659	9	ADc06860	Plasmid p
XX	c 43	92.2	90.4	660	9	ADc06864	Plasmid p
PR 30-AUG-1999; 99DE-01041186.	c 44	92.2	90.4	2591	6	ABK88866	Topoisome
XX	c 45	92.2	90.4	2591	10	ADe83789	Plasmid p
XX							
FA (DROE/) DROEGE P.							
PI Droege P;							
XX WPI; 2001-246016/26.							
DR							
XX							
PT Sequence-specific recombination of DNA in eukaryotes, useful particularly							
for somatic cell gene therapy, uses an integrase to effect recombination							
between att sites.							
XX							
Claim 3; Page 14; 24pp; German.							
XX							
CC This invention describes a novel sequence-specific recombination (SSR) of							
DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,							
II) into a cell, using an integrase (Int) to effect SSR. The invention							
also describes (1) a nucleic acid comprising a 243 base pair sequence							
(III), fully defined in the specification, or its derivatives; and (2)							
vector containing (III), or its derivatives, plus a therapeutic gene, or							
its derivatives. The method is particularly used in somatic gene therapy							
in humans and animals, but can be applied more generally for gene							
transfer to animal or plant cells. The method is simple and controllable,							
and provides stable and targeted integration of selected DNA sequences							
XX							

SQ Sequence 102 BP; 35 A; 16 C; 13 G; 38 T; 0 U; 0 Other;
Query Match 100.0%; Score 102; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.5e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATACCTAAGTGGCATTATATAAAAGCATTGCTATCAATTTGTCACAG 60
DB 1 CTGCTTTTATACCTAAGTGGCATTATATAAAAGCATTGCTATCAATTTGTCACAG 60
QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
DB 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
RESULT 2
AAT30737
ID AAT30737 standard; DNA; 2408 BP.
XX AAT30737;
AC AAT30737;
DT 20-OCT-1996 (first entry)
XX Rat cryptdin 2 gene.
DE
XX Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation;
KW antinflammatory; inflammatory bowel disease; pancreatitis; cancer;
KW tumour; ileitis; ds.
XX Rattus sp.
OS
XX
FH Key Location/Qualifiers
FT exon 1. .1345
FT /tag= a
FT /codon_start= 1174. .1176
FT /note= "exon 1 codes for the 5' untranslated region and
FT cryptdin-1 prepro sequence"
FT intron 1345. .1930
FT /tag= b
FT exon 1931. .2408
FT /tag= c
FT /note= "exon 2 codes for cryptdin-2 and 3' untranslated
FT region"
XX
PN WC9616075-AL.
XX
XX 30-MAY-1996.
XX
XX 05-OCT-1995; 95WO-US013328.
XX
XX 18-NOV-1994; 94US-00342268.
XX
XX (REGC) UNIV CALIFORNIA.
PA (SHRI-) SHRINER'S HOSPITAL FOR CRIPPLED CHILDREN.
XX
XX Selsted ME, Ouellette AJ;
PI
XX WPI; 1996-268527/27.
DR P-PSDB; AAR98787, AAR98792.
XX
XX New isolated cryptdin peptide(s) - which have antimicrobial activity,
PT used partic. in the detection and treatment of inflammatory pathologies.
PT
XX Claim 31; Page 64-65; 103pp; English.
PS
XX The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of
CC cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity
CC against a broad range of intestinal and opportunistic pathogens. Rat
CC cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated
CC from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2
CC gene, or corresponding cDNA (see also T30734), can be used to produce
CC large amounts of cryptdin-2 for use in treating inflammatory pathologies
CC of the intestine

XX
SQ Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;
Query Match 100.0%; Score 102; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 6.5e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATACCTAAGTGGCATTATATAAAAGCATTGCTATCAATTTGTCACAG 60
DB 408 CTGCTTTTATACCTAAGTGGCATTATATAAAAGCATTGCTATCAATTTGTCACAG 467
QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
DB 468 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 509
RESULT 3
ABN81284
ID ABN81284 standard; DNA; 3049 BP.
XX ABN81284;
AC ABN81284;
DT 22-AUG-2002 (first entry)
XX Beet promoter polynucleotide SEQ ID NO 4.
DE Beet promoter polynucleotide SEQ ID NO 4.
XX Beet; promoter; carbohydrate metabolism; invertase inhibitor;
KW fructosyl transferase; levan sucrase; nitrogen transporter protein;
KW pathogen resistance; plant; transgenic; ds.
XX Beta vulgaris.
OS
XX
FH Key Location/Qualifiers
FT Promoter 1. .2998
FT /tag= a
FT TATA_signal 2877. .2883
FT /tag= c
FT mRNA 2928. .3049
FT /tag= b
XX
XX BP1207204-AL.
PN
XX 22-MAY-2002.
XX
XX 16-NOV-2000; 2000EP-00124989.
XX
XX 16-NOV-2000; 2000EP-00124989.
XX (KWSS-) KWS SAAT AG.
XX
XX Hehl R, Kloos D, Stahl DJ;
PI
XX WPI; 2002-437465/47.
DR
XX New tissue-specific promoters from Beta vulgaris, useful e.g. for
PT altering carbohydrate metabolism, express transgenes selectively in roots
PT or aerial parts.
XX
XX Claim 1; Page 30-31; 57pp; German.
PS
XX The invention relates to a promoter (A) that is: (i) any of the sequences
CC ABN81281-ABN81284; (ii) the complement of (i); or (iii) a sequence that
CC hybridises to (ii). (A) are used, specifically in Beta vulgaris, to
CC control expression of transgenes, particularly to alter carbohydrate
CC metabolism; reduce loss of storage substances; express invertase
CC inhibitor, fructosyl transferase, levan sucrase or genes that encode
CC transporter proteins for nitrogen compounds, or increase resistance to,
CC or tolerance of, pathogens. (A) provide tissue-specific transgene
CC expression, either in roots or above-ground parts, so avoid pleiotropic
CC effects, e.g. when expressing invertase inhibitor
XX
XX Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;
SQ

```

Query Match      100.0%; Score 102; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAGTTCGCAATATATAAAAGCAATGCTTATCAATTTGTTGCAACG 60
DB 2398 CTGCTTTTATACAGTTCGCAATATATAAAAGCAATGCTTATCAATTTGTTGCAACG 2457

QY 61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTGATTTC 102
DB 2458 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTGATTTC 2499

RESULT 4
AAV34987
ID AAV34987 standard; DNA; 3484 BP.
XX AC AAV34987;
XX 17-OCT-2003 (revised)
XX 28-SEP-1998 (first entry)
Arabidopsis nematode feeding site-preferential promoter.
Promoter; nematode feeding site; root knot nematode; cyst nematode;
Meloidogyne incognita; Heterodera schachtii; Globodera pallida;
transgenic plant; pest resistance; crop protection; ds.
Arabidopsis thaliana; ecotype C24.
XX Key Location/Qualifiers
XX CDS 3482
XX /*tag= a
XX /codon_start= 3482. 3484
XX WO9822599-A1.
XX 28-MAY-1998.
XX 18-NOV-1997; 97MO-EP006472.
XX 18-NOV-1996; 96EP-00203213.
XX (MOGE-) MOGEN INT NV.
XX Ohl SA, Van Der Lee FM, Goddijn OJM, Klap J, Sijmons PC;
XX WPI; 1998-312484/27.
XX New Arabidopsis thaliana DNA promoter - useful for, e.g. generating plant
XX reduced susceptibility to plant parasitic nematodes.
XX Claim 1; Page 22-24; 47pp; English.
XX This DNA fragment obtainable from Arabidopsis thaliana is capable of
XX promoting root knot and cyst nematode-inducible transcription of an
XX associated DNA sequence when reintroduced into a plant. The promoterless
XX GUS construct binary vector pMOG553 was mobilised by triparental mating
XX to Agrobacterium tumefaciens MOG101 and the resulting strain was used for
XX Arabidopsis root transformation. Line pMOG553#25 was identified as a line
XX which showed strong GUS expression inside syncytia and giant cells
XX induced by the cyst nematode Heterodera schachtii and the root knot
XX nematode Meloidogyne incognita, respectively. Promoter tags from line
XX pMOG553#25 were sequenced. The claimed DNA fragment is nematode feeding
XX site-specific. Also claimed are: (1) a portion or variant of the above
XX sequence capable of promoting root knot and cyst nematode inducible
XX transcription of an associated DNA sequence when reintroduced into a
XX plant; (2) a chimeric DNA sequence comprising a DNA fragment as above
XX plus a DNA sequence which is not naturally under its transcriptional
XX control, and which causes the production of a plant cell-disruptive
XX substance, preferably barnase; (3) a replicon comprising the chimeric DNA
XX sequence of (2), or the above DNA and at least 1 restriction endonuclease
XX recognition site; (4) a microorganism containing the replicon of (3); (5)

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a plant cell having incorporated into its genome the chimeric DNA of (2);
(6) a root system of a plant consisting of the cells of (5); (7) a plant
consisting of the cells of (5), preferably a dicotyledonous plant,
especially a potato plant; (8) a plant grafted onto the root system of
(6); (9) a part of a plant, selected from seeds, flowers, tubers, roots,
leaves, fruits, pollen and wood, obtained from the plant of (7) or (8),
and (10) a crop consisting of the plants of (7) or (8). The DNA fragment
can be used to identify subfragments capable of promoting transcription
of an associated DNA sequence in a plant. It can also be used for making
hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be
used for transforming plants (all claimed). The DNA sequence can be used
to reduce the susceptibility of a plant to parasitic nematodes. (Updated
on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 U; 0 Other;
Query Match      100.0%; Score 102; DB 2; Length 3484;
Best Local Similarity 100.0%; Pred. No. 6.8e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAGTTCGCAATATATAAAAGCAATGCTTATCAATTTGTTGCAACG 60
DB 420 CTGCTTTTATACAGTTCGCAATATATAAAAGCAATGCTTATCAATTTGTTGCAACG 479

QY 61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTGATTTC 102
DB 480 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTGATTTC 521

RESULT 5
AAV44332
ID AAV44332 standard; DNA; 3757 BP.
XX AC AAV44332;
XX 24-NOV-1998 (first entry)
XX Murine mMCP-6 zymogen gene.
XX MCP-6 zymogen; mouse; mast cell protease 6; mMCP-7; tryptase-7;
XX blood clot; anticoagulant; myocardial infarction; reocclusion;
XX thromboembolism; cerebral embolism; thrombosis; therapy; ss.
XX Mus sp.
XX Key Location/Qualifiers
XX CDS 1803..3098
XX /*tag= a
XX /note= "contains introns"
XX exon 1803..1872
XX /*tag= b
XX /number= 1
XX intron 1873..2011
XX /*tag= c
XX /number= 1
XX exon 2012..2177
XX /*tag= d
XX /number= 2
XX intron 2178..2297
XX /*tag= e
XX /number= 2
XX exon 2298..2563
XX /*tag= f
XX /number= 3
XX intron 2564..2696
XX /*tag= g
XX /number= 3
XX exon 2697..2860
XX /*tag= h
XX /number= 4
XX intron 2861..2933
XX /*tag= i
XX /number= 4

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FT exon          2934..3098
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FT              /number= 5
XX
XX WO9824886-A1.
XX
XX 11-JUN-1998.
XX
XX 25-NOV-1997; 97WO-US021620.
XX
XX 04-DEC-1996; 96US-0032354P.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Stevens RL;
XX
XX WPI; 1998-333308/29.
XX P-PSDB; AAW64242.
XX
XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
XX are used to treat clot formation in e.g. myocardial infarction,
XX reocclusion following angioplasty or pulmonary thrombo-embolism.
XX
XX Disclosure; Page 68-69; 92pp; English.
XX
XX This nucleotide sequence includes a coding region for mouse mast cell
XX protease 6 (mMCP-6, see AAW64242). The invention provides: compositions
XX comprising an isolated tryptase-7 (such as mMCP-7, see AAW64233); a
XX method for treating a blood clot by administering a nucleic acid molecule
XX that codes for a tryptase-7, or an expression product; a nucleic acid
XX encoding a serine protease (SP); and a method of producing a mature SP.
XX Tryptase-7 polypeptides can be used for treating disorders mediated by
XX undesirable thrombus clot formation such as myocardial infarction and
XX reocclusion following angioplasty of blood clots associated with
XX pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
XX vein and peripheral arterial thrombosis
XX
XX Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 102; DB 2; Length 3757;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-19;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
XX |||||||
XX 374 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
XX
XX QY 61 AACAGGTCATCTACGTCACAAATAAAATCAATTATTGATTTC 102
XX |||||||
XX 434 AACAGGTCATCTACGTCACAAATAAAATCAATTATTGATTTC 475
XX
XX RESULT 6
XX AAV42708
XX ID AAV42708 standard; cDNA; 3757 BP.
XX
XX AC AAV42708;
XX
XX XX 27-OCT-1998 (first entry)
XX
XX DE Mouse mast cell protease (mMCP-6) nucleic acid sequence.
XX
XX KW Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
XX tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
XX antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
XX hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
XX inflammatory skin condition; ss.
XX
XX OS Mus sp.
XX
XX XX WO9833812-A1.
XX
XX XX 06-AUG-1998.

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XX 30-JAN-1998; 98WO-US001865.
XX
XX 05-FEB-1997; 97US-0037090P.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Stevens RL, Huang C;
XX
XX WPI; 1998-437390/37.
XX
XX Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
XX inflammatory disorders e.g. asthma.
XX
XX Disclosure; Page 42-43; 69pp; English.
XX
XX This represents the cDNA sequence of the mouse mast cell protease (mMCP-
XX 6). The invention provides sequences shown in AAW63160 to AAW63169 that
XX are inhibitors of mMCP-6. These peptides which are tryptase-6 complex
XX inhibitors, can be used for treating a mast cell-mediated inflammatory
XX disorder. The inhibitors can be used to treat inflammatory disorders
XX including asthma, allergic rhinitis, urticaria and antioedema, eczematous
XX dermatitis (atopic dermatitis), hyperproliferative skin disease,
XX anaphylaxis, peptic ulcers, inflammatory bowel disorder,
XX hyperresponsiveness and inflammatory skin conditions
XX
XX Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 102; DB 2; Length 3757;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-19;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
XX |||||||
XX 374 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
XX
XX Db 61 AACAGGTCATCTACGTCACAAATAAAATCAATTATTGATTTC 102
XX |||||||
XX 434 AACAGGTCATCTACGTCACAAATAAAATCAATTATTGATTTC 475
XX
XX RESULT 7
XX AAV23239/C
XX ID AAV23239 standard; DNA; 5349 BP.
XX
XX AC AAV23239;
XX
XX XX 17-JUL-1998 (first entry)
XX
XX DE T-DNA of pTTS24.
XX
XX KW Barstar; barnase inhibitor; fertility restoration; male-sterile line;
XX plasmid pTTS24; T-DNA; ds.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX misc_feature complement(1..25)
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XX FT /label= RB
XX FT /note= "right boarder"
XX FT complement(98..331)
XX FT /*tag= b
XX FT /label= 3'_g7
XX FT /note= "region containing 3' untranslated end of
XX Agrobacterium T-DNA gene 7"
XX CDS 332..883
XX FT /*tag= c
XX FT /label= bar
XX FT /note= "region coding for phosphinothricin acetyl
XX transferase"
XX FT complement(884..2258)
XX FT /*tag= d

```

```

FT      /label= P35S
FT      /note= "35S promoter of Cauliflower Mosaic Virus"
FT      2281..3969
FT      /tag= e
FT      /label= PE1
FT      /note= "promoter of E1 gene of rice (W09213956)"
FT      3970..4245
FT      /tag= f
FT      /product= "improved_barstar"
FT      4246..4577
FT      /tag= g
FT      /label= 3' _chs
FT      /note= "region containing 3' untranslated end of chalcone
FT      synthase gene"
FT      complement(5325..5349)
FT      /tag= h
FT      /note= "T-DNA left border"
PN      W09810081-A2.
XX
XX      12-MAR-1998.
PD
PF      01-SEP-1997; 97WO-EP004739.
XX
XX      03-SEP-1996; 96EP-00202446.
XX
XX      (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX      Michiels F, Williams M;
XX      WPI; 1998-193630/17.
XX
XX      DNA encoding an improved barstar protein - used to restore fertility in
XX      male-sterile plant lines.
XX
XX      Example 4; Page 41-43; 54pp; English.
XX
XX      The present sequence was used in the preparation of an improved Bacillus
XX      amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to
XX      restore fertility to male-sterile lines. The DNA sequence encoding the
XX      improved barstar, leads to increased barstar production in tapetum cells,
XX      due to improved translation, and possibly protein stability
XX
XX      Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 102; DB 2; Length 5349;
XX      Best Local Similarity 100.0%; Pred. No. 7.1e-19;
XX      Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTGCTTTTATACTAAGTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db      4885 CTGCTTTTATACTAAGTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 4826

Qy      61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTTC 102
Db      4825 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTTC 4784

RESULT 8
AAV23242/c
ID      AAV23242 standard; DNA; 5611 BP.
XX
XX      AAV23242;
XX
XX      17-JUL-1998 (first entry)
XX      Plasmid pLH48.
XX
XX      Barstar; barnase inhibitor; fertility restoration; male-sterile line;
XX      plasmid pLH48; circular; gb.
XX      Synthetic.
XX

```

```

PH      Key      Location/Qualifiers
FT      3'UTR      complement(39..317)
FT      /tag= a
FT      /label= 3' _nos
FT      /note= "region containing 3' untranslated end of nopaline
FT      synthase gene of Agrobacterium T-DA"
FT      complement(318..869)
FT      /tag= b
FT      /label= bar
FT      /note= "region coding for phosphinothricin acetyl
FT      transferase"
FT      complement(870..1702)
FT      /tag= c
FT      /label= P35S
FT      /note= "35S promoter of Cauliflower Mosaic Virus"
FT      1740..2284
FT      /tag= d
FT      /label= PTA29
FT      /note= "promoter of TA29 gene of Nicotiana tabacum"
FT      2285..2560
FT      /tag= e
FT      /product= "improved_barstar"
FT      2561..2892
FT      /tag= f
FT      /label= 3' _chs
FT      /note= "region containing 3' untranslated end of chalcone
FT      synthase gene"
FT      FT
XX
XX      W09810081-A2.
XX
XX      12-MAR-1998.
XX
XX      01-SEP-1997; 97WO-EP004739.
XX
XX      03-SEP-1996; 96EP-00202446.
XX
XX      (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX      Michiels F, Williams M;
XX      WPI; 1998-193630/17.
XX
XX      DNA encoding an improved barstar protein - used to restore fertility in
XX      male-sterile plant lines.
XX
XX      Disclosure; Page 45-48; 54pp; English.
XX
XX      The present sequence was used in the preparation of an improved Bacillus
XX      amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to
XX      restore fertility to male-sterile lines. The DNA sequence encoding the
XX      improved barstar, leads to increased barstar production in tapetum cells,
XX      due to improved translation, and possibly protein stability
XX
XX      Sequence 5611 BP; 1389 A; 1342 C; 1353 G; 1527 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 102; DB 2; Length 5611;
XX      Best Local Similarity 100.0%; Pred. No. 7.2e-19;
XX      Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTGCTTTTATACTAAGTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db      3200 CTGCTTTTATACTAAGTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 3141

Qy      61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTTC 102
Db      3140 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTTC 3099

RESULT 9
AAQ50319
ID      AAQ50319 standard; DNA; 201 BP.
XX
XX      AAQ50319;
AC

```

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XX 27-APR-1994 (first entry)
XX Detection probe 11.
XX Probe; chip; cell; detection; label; capture probe; ss.
XX Synthetic.
XX JP05236997-A.
XX 17-SEP-1993.
XX 28-FEB-1992; 92JP-00042829.
XX 28-FEB-1992; 92JP-00042829.
XX (HITA ) HITACHI LTD.
XX WPI; 1993-330600/42.
XX Chip for capturing polynucleotide - has several different complementary
XX probes fixed on cells at different sites on single tip.
XX Disclosure; Page 8; 10pp; Japanese.
XX The sequences given in AAQ0309-26 are probes which were used on a chip
XX for capturing a number of target polynucleotides. A group of these probes
XX may be attached on cells which form part of a single chip. The
XX oligonucleotides to be detected are labelled and are complementary to the
XX set of capture probes used. The detection chip may be used to detect a
XX number of different polynucleotides concurrently
XX Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 U; 0 Other;
SQ Query Match 98.4%; Score 100.4; DB 2; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.3e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX 1 CTGCTTTTATATAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
XX 43 CAGCTTTTATATAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 102
XX 61 AACAGTCTACTATCACTCAAAATAAATCAATTTGTTGTTTC 102
XX 103 AACAGTCTACTATCACTCAAAATAAATCAATTTGTTGTTTC 144
XX
XX RESULT 10
XX AAF61418
XX ID AAF61418 standard; DNA; 243 BP.
XX AC AAF61418;
XX 05-JUN-2001 (first entry)
XX Bacteriophage lambda attP DNA fragment.
XX Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
XX targeted integration; attP; ds.
XX Bacteriophage lambda.
XX DE19941186-A1.
XX 01-MAR-2001.
XX 30-AUG-1999; 99DE-01041186.
XX 30-AUG-1999; 99DE-01041186.
XX (DROE/) DROEGE P.
XX

```

```

PI Droegge P;
XX WPI; 2001-246016/26.
XX Sequence-specific recombination of DNA in eukaryotes, useful particularly
XX for somatic cell gene therapy, uses an integrase to effect recombination
XX between att sites.
XX Claim 2; Page 13; 24pp; German.
XX This invention describes a novel sequence-specific recombination (SSR) of
XX DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
XX II) into a cell, using an integrase (Int) to effect SSR. The invention
XX also describes (1) a nucleic acid comprising a 243 base pair sequence
XX (III), fully defined in the specification, or its derivatives; and (2)
XX its derivatives. The method is particularly used in somatic gene therapy
XX in humans and animals, but can be applied more generally for gene
XX transfer to animal or plant cells. The method is simple and controllable,
XX and provides stable and targeted integration of selected DNA sequences
XX
XX Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
SQ Query Match 98.4%; Score 100.4; DB 4; Length 243;
Best Local Similarity 99.0%; Pred. No. 1.4e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX 1 CTGCTTTTATATAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
XX 142 CAGCTTTTATATAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
XX 61 AACAGTCTACTATCACTCAAAATAAATCAATTTGTTGTTTC 102
XX 202 AACAGTCTACTATCACTCAAAATAAATCAATTTGTTGTTTC 243
XX
XX RESULT 11
XX ACC85316
XX ID ACC85316 standard; DNA; 248 BP.
XX AC ACC85316;
XX 18-SEP-2003 (first entry)
XX Recombinase lambda integrase attP DNA recognition sequence.
XX Vegetable plastid transformation; transgenic; recognition sequence;
XX plant; site-specific integration; nutrition; seed production;
XX chemical production; ds.
XX Unidentified.
XX WO2003054201-A1.
XX 03-JUL-2003.
XX 16-DEC-2002; 2002WO-EP014303.
XX 20-DEC-2001; 2001DE-01063159.
XX (SUNG-) SUNGENE GMBH & CO KGAA.
XX Biesgen C;
XX WPI; 2003-541820/51.
XX Site-specific integration of DNA into plastid DNA, useful for making
XX transgenic plants used e.g. as food, by recombinase-mediated insertion.
XX Disclosure; Page 35; 164pp; German.
XX The present invention relates to a method for the site-specific
XX integration of a DNA sequence into the plastid DNA of a plant or its
XX

```

CC derived cells. Transgenic plants in which a DNA sequence has been
 CC integrated, also their cell cultures, organs, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a recognition sequence shown in the exemplification
 CC of the invention
 CC
 XX Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;
 XX
 Query Match 98.4%; Score 100.4; DB 8; Length 248;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
 Db 147 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 206
 QY 61 AACAGGTCATCTATCAGTCAAAATAAATCAATTTATTTGATTTC 102
 Db 207 AACAGGTCATCTATCAGTCAAAATAAATCAATTTATTTGATTTC 248

RESULT 12
 AC44676
 ID ACC44676 standard; DNA; 282 BP.
 XX
 AC ACC44676;
 XX
 DT 29-MAY-2003 (first entry)
 XX
 XX Murine rDNA PCR primer SEQ ID NO:72.
 DE
 XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; gene; ds.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN WO200297059-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US017452.
 XX
 PR 30-MAY-2001; 2001US-0294758P.
 PR 21-MAR-2002; 2002US-0366891P.
 XX
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA
 XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;
 PI
 XX WPI; 2003-140461/13.
 DR
 XX Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest.
 XX
 XX Example 2; Page 207; 272pp; English.

CC The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a

CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
 XX
 Query Match 98.4%; Score 100.4; DB 7; Length 282;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
 Db 156 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 215
 QY 61 AACAGGTCATCTATCAGTCAAAATAAATCAATTTATTTGATTTC 102
 Db 216 AACAGGTCATCTATCAGTCAAAATAAATCAATTTATTTGATTTC 257

RESULT 13
 ABT16636
 ID ABT16636 standard; DNA; 282 BP.
 XX
 AC ABT16636;
 XX
 DT 03-APR-2003 (first entry)
 XX
 XX Artificial plant chromosome related oligo SEQ ID No 48.
 DE
 XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 PN WO200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US017451.
 XX
 PR 30-MAY-2001; 2001US-0294687P.
 PR 04-JUN-2001; 2001US-0296329P.
 XX
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 XX Perez C, Fabijanski SF, Perkins E;
 XX
 XX WPI; 2003-140436/13.

Producing artificial chromosome by introducing a nucleic acid into plant
 cell, selecting artificial chromosome that has one or more repeat regions
 with equivalent amounts of euchromatic and heterochromatic nucleic acids.
 XX
 XX Disclosure; Page 263-264; 269pp; English.

CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and

CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention
 XX
 SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;

Query Match 98.4%; Score 100.4; DB 7; Length 282;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTGGCATTATATAAAGCAATTCCTTATCAATTTGTGCAACG 60
 |
 Db 156 CAGCTTTTATACAAAGTGGCATTATATAAAGCAATTCCTTATCAATTTGTGCAACG 215
 |
 QY 61 AACAGTCACTATCAGTCAAAATAAATCAATCATTATTGATTTC 102
 |
 Db 216 AACAGTCACTATCAGTCAAAATAAATCAATCATTATTGATTTC 257
 |

RESULT 14
 AAF79770
 ID AAF79770 standard; DNA; 610 BP.
 AC AAF79770;
 XX
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Bacteriophage lambda attachment P region.
 XX
 KW Attachment P region; attP; recombination; marker gene removal; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO200121780-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 15-SEP-2000; 2000WO-GH003543.
 XX
 PR 17-SEP-1999; 99GB-00021937.
 XX
 PA (UYLE-) UNIV LEEDS.
 XX
 PI Meyer P, Zubko E;
 XX
 DR WPI; 2001-266072/27.
 XX
 PT Removing a part of a transgene which has been integrated into a genome
 PT comprises inducing intrachromosomal homologous recombination between the
 PT attachment P regions of bacteriophage lambda flanking the transgene.
 XX
 PS Claim 8; Fig 3D; 25pp; English.
 XX

The present invention describes a method of removing a transgene marker
 by flanking the transgene with a bacteriophage lambda attachment P (attP)
 region and inducing homologous recombination between attP regions so that
 the transgene is removed. This is useful in the production of transgenic
 plants with less risk of inter-species transmission of marker genes,
 CC which often encode proteins associated with, for example, herbicide and
 CC antibiotic resistance. The present sequence is the attP coding region
 XX
 SQ Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;

Query Match 98.4%; Score 100.4; DB 5; Length 610;
 Best Local Similarity 99.0%; Pred. No. 1.5e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTGGCATTATATAAAGCAATTCCTTATCAATTTGTGCAACG 60
 |
 Db 280 CAGCTTTTATACAAAGTGGCATTATATAAAGCAATTCCTTATCAATTTGTGCAACG 339
 |
 QY 61 AACAGTCACTATCAGTCAAAATAAATCAATCATTATTGATTTC 102
 |
 Db 340 AACAGTCACTATCAGTCAAAATAAATCAATCATTATTGATTTC 381
 |

RESULT 15
 ABQ80306
 ID ABQ80306 standard; DNA; 1469 BP.
 XX
 AC ABQ80306;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Lambda fragment in plasmid DNA.
 XX
 KW Primer; PCR; amplify; lambda phage; primer material; insertion; SNP;
 KW deletion; single nucleotide polymorphism; sequencing; diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003027991-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-JP009766.
 XX
 PR 25-SEP-2001; 2001JP-00291249.
 XX
 PA (DNAF-) DNAFORM KK.
 PA (RIKE-) RIKEN KK.
 XX
 PI Hayashizaki Y;
 XX
 DR WPI; 2003-354676/33.
 XX

Printed material useful as a delivery and storage system for oligomer
 and/or polymer, comprises a support having an oligomer and/or polymer
 applied on it.
 Example 1; Page 31-32; 91pp; English.

The sequences given in ABQ80304-05 are primers which were used to amplify
 DNA for use in the material of the invention. The primers amplify a 1377
 bp portion of lambda phage DNA contained in a plasmid. The amplified
 sequence (ABQ80306) was attached to the primer material of the invention
 which comprises at least one support having at least one oligomer and/or
 polymer applied on it. The printed material is useful in a method for
 synthesising DNA where the product of amplification and/or ligation is
 cDNA and/or full-length cDNA which is recovered and used for
 determination of nucleotide insertion/deletion, single nucleotide
 polymorphism (SNP) and sequencing analysis, in a diagnostic method for
 determination of nucleotide insertion/deletion, or SNP analysis.
 CC Optionally, the cDNA and/or full-length cDNA is useful for the peptide,
 CC polypeptide or protein expression. The printed material is useful in
 CC research applications, or for providing scientists with oligomer and/or
 CC polymers from the printed materials easily and immediately. From the
 CC printed material, at least an oligomer and/or polymer can be obtained
 CC immediately and directly, without need to make a request for it. The
 CC oligomers and/or polymers can be delivered and stored easily with reduced
 CC labour and time while eliminating the need to use special equipment or
 CC facilities. Thus, the printed material is a quick, efficient and
 CC inexpensive sample delivery system

Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;

Query Match 98.4%; Score 100.4; DB 7; Length 1469;
 Best Local Similarity 99.0%; Pred. No. 1.7e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATAAGTTGGCAATTATAAAAGCATTGCTTATCAATTGTTGCAAG 60
 Db |||||
 949 CAGCTTTTATATAAGTTGGCAATTATAAAAGCATTGCTTATCAATTGTTGCAAG 1008
 QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
 Db |||||
 1009 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 1050

Search completed: September 9, 2004, 18:05:40
 Job time : 117.156 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11 ; Search time 22.4903 Seconds
(without alignments)
2516.866 Million cell updates/sec

Title: US-10-082-772B-3

Perfect score: 102

Sequence: 1 ctgctttttatactaagtt.....taaaatcattattgatttc 102

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	2408	1	US-08-486-013-69
2	102	100.0	2408	2	US-08-482-279-69
3	102	100.0	2408	2	US-08-342-268-69
4	102	100.0	2408	3	US-09-015-988-69
5	102	100.0	2408	4	US-09-397-386-69
6	102	100.0	3484	4	US-09-308-090-1
7	102	100.0	3484	4	US-09-380-090A-1
8	102	100.0	3757	2	US-09-016-366A-13
9	102	100.0	3757	2	US-08-978-404B-19
10	102	100.0	5349	4	US-09-068-101-7
11	102	100.0	5611	4	US-09-068-101-10
12	100.4	98.4	201	1	US-08-021-667A-18
13	100.4	98.4	201	1	US-08-410-544-18
14	100.4	98.4	201	1	US-08-728-785A-18
15	100.4	98.4	4909	3	US-08-556-978B-78
16	100.4	98.4	6043	4	US-09-630-929-4
17	100.4	98.4	7652	1	US-07-590-988A-1
18	80.2	78.6	228	4	US-09-107-532A-667
19	62	60.8	38584	4	US-09-453-702B-50
20	41.6	40.8	9827	4	US-09-453-702B-66
21	32.2	31.6	11049	4	US-10-204-708-24
22	30.6	30.0	675	4	US-09-543-681A-3694
23	30.4	29.8	786431	4	US-09-751-389-3
24	30.2	29.6	4429	1	US-08-308-872B-3
25	30	29.4	2004	4	US-08-956-171E-269
26	29.6	29.0	4140	3	US-08-894-731-2
27	28.8	28.2	4359	2	US-08-566-398-23
C 28	28.8	28.2	28.8	28.2	US-08-392-459-21
C 29	28.8	28.2	28.8	28.2	US-09-854-799-21
C 30	28.8	28.2	28.8	28.2	PCT-US91-08525-21
C 31	28.8	28.2	28.8	28.2	PCT-US93-04384-1
C 32	28.6	28.0	4500	1	US-08-308-872B-1
C 33	28.2	27.6	602	4	US-08-916-246-1
C 34	28.2	27.6	654	4	US-09-134-001C-2801
C 35	28.2	27.6	580073	4	US-08-545-528D-1
C 36	28	27.5	483	4	US-09-621-976-14383
C 37	28	27.5	611	3	US-09-385-982-357
C 38	28	27.5	2099	1	US-08-299-849B-25
C 39	28	27.5	2099	2	US-08-142-368A-25
C 40	28	27.5	2099	3	US-08-967-727-25
C 41	28	27.5	2099	3	US-08-037-230D-25
C 42	28	27.5	2099	4	US-09-583-850-25
C 43	28	27.5	2099	4	US-09-579-197-25
C 44	28	27.5	2099	4	US-09-404-026-25
C 45	28	27.5	2099	4	US-09-312-464-25

ALIGNMENTS

RESULT 1

US-08-486-013-69
; Sequence 69, Application US/08486013
; Patent No. 5731149
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptidin Peptides and Methods
; TITLE OF INVENTION: Of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,013
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-486-013-69

Query Match 100.0%; Score 102; DB 1; Length 2408;

Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

QY 1 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 408 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 2

US-08-482-279-69
; Sequence 69, Application US/08482279
; Patent No. 5840498
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,279
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-279-69

Query Match 100.0%; Score 102; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

QY 1 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 408 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 3

US-08-342-268-69
; Sequence 69, Application US/08342268
; Patent No. 5844072
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,268
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-342-268-69

Query Match 100.0%; Score 102; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

QY 1 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 408 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 4

US-09-015-968-69
; Sequence 69, Application US/09015968
; Patent No. 6057425
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-015-968-69

Query Match 100.0%; Score 102; DB 3; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db 408 CTGCTTTTATACAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 61 AACAGGTCACATCACTAGTCAAAATATAAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCACTAGTCAAAATATAAAATCAATTTGATTTC 509

RESULT 5

US-09-397-386-69
Sequence 69, Application US/09397386
Patent No. 6300470

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptidin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-397-386-69

Query Match 100.0%; Score 102; DB 4; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db 408 CTGCTTTTATACAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467

QY 61 AACAGGTCACATCACTAGTCAAAATATAAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCACTAGTCAAAATATAAAATCAATTTGATTTC 509

RESULT 6

US-09-308-090-1
Sequence 1, Application US/09308090
Patent No. 6395963

GENERAL INFORMATION:

APPLICANT: Ohl, Stephan
APPLICANT: Van der Lee, Frederique
APPLICANT: Goddijn, Oscar
APPLICANT: Klap, Joke
APPLICANT: Sijmons, Peter
TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
FILE REFERENCE: MOG 57680
CURRENT APPLICATION NUMBER: US/09/308,090
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/EP97/06472
EARLIER FILING DATE: 1997-11-18
EARLIER APPLICATION NUMBER: EP 96203213.2
EARLIER FILING DATE: 1996-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 3484
TYPE: DNA
ORGANISM: Arabidopsis thaliana

```
;
; NAME/KEY: CDS
; LOCATION: (3482) .. (3484)
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-090A-1

Query Match      100.0%; Score 102; DB 4; Length 3484;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
   |||||||
Db 420 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 61 AACAGTCACTATCACTCAAAATAAAATCAATTATTGATTC 102
   |||||||
Db 480 AACAGTCACTATCACTCAAAATAAAATCAATTATTGATTC 521

RESULT 7
US-09-380-090A-1
; Sequence 1, Application US/09380090A
; Patent No. 6555529
; GENERAL INFORMATION:
; APPLICANT: OHL, Stephan Andreas
; SIMONS, Peter Christiaan
; KLEIN-VAN DER LEE, Frederique
; Marianne
; GODDION, Oscar
; Klap, Joke
; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hale and Dorr LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09380,090A
; FILING DATE: 17-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06472
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: EP 96203213.2
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: SYN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3484 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; STRAIN: C24
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 3481..3484
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-090A-1

Query Match      100.0%; Score 102; DB 4; Length 3484;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
   |||||||
Db 420 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 61 AACAGTCACTATCACTCAAAATAAAATCAATTATTGATTC 102
   |||||||
Db 480 AACAGTCACTATCACTCAAAATAAAATCAATTATTGATTC 521

RESULT 8
US-09-016-366A-13
; Sequence 13, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3757 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-016-366A-13

Query Match      100.0%; Score 102; DB 2; Length 3757;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
   |||||||
Db 374 CTGCTTTTATACAAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
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QY 61 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 102
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 434 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 475
 Db |||||||||||||||||||||||||||||||||||||||||||||

RESULT 9

US-08-978-404B-19
 ; Sequence 19, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: NAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3757 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-978-404B-19

Query Match 100.0%; Score 102; DB 2; Length 3757;
 Best Local Similarity 100.0%; Pred. No. 4.3e-20;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 374 CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG 433
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 61 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 102
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 434 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 475
 Db |||||||||||||||||||||||||||||||||||||||||||||

RESULT 10

US-09-068-101-7/c
 ; Sequence 7, Application US/09068101
 ; Patent No. 6372960
 ; GENERAL INFORMATION:
 ; APPLICANT: PLANT GENETIC SYSTEMS N.V.
 ; TITLE OF INVENTION: Improved Barstar Gene
 ; FILE REFERENCE: 2121-139P
 ; CURRENT APPLICATION NUMBER: US/09/068,101
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: EP 96202446.9

; EARLIER FILING DATE: 1996-09-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 5349
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
 ; OTHER INFORMATION: acid, "T-DNA of pTTS243"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(11)..(25))
 ; OTHER INFORMATION: label = RB, "T-DNA right border"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(98)..(331))
 ; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
 ; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(332)..(883))
 ; OTHER INFORMATION: label = bar, "region coding for phosphinotricin
 ; OTHER INFORMATION: acetyl transferase"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(884)..(2258))
 ; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
 ; OTHER INFORMATION: Virus"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2281)..(3969)
 ; OTHER INFORMATION: label = PEI, "promoter of EI gene of rice (WO
 ; OTHER INFORMATION: 92/13956)"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (3970)..(4245)
 ; OTHER INFORMATION: label = synb*, "improved barstar DNA"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4246)..(4577)
 ; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
 ; OTHER INFORMATION: end of chalcone synthase gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(5325)..(5349))
 ; OTHER INFORMATION: label = LB, "T-DNA left border"
 ; US-09-068-101-7

Query Match 100.0%; Score 102; DB 4; Length 5349;
 Best Local Similarity 100.0%; Pred. No. 4.6e-20;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 4885 CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG 4826
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 61 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 102
 Db |||||||||||||||||||||||||||||||||||||||||||||

QY 4825 AACAGGTCACATCATCAGTCAAAATAAATCATTTTGGATTTC 4784
 Db |||||||||||||||||||||||||||||||||||||||||||||

RESULT 11

US-09-068-101-10/c
 ; Sequence 10, Application US/09068101
 ; Patent No. 6372960
 ; GENERAL INFORMATION:
 ; APPLICANT: PLANT GENETIC SYSTEMS N.V.
 ; TITLE OF INVENTION: Improved Barstar Gene
 ; FILE REFERENCE: 2121-139P
 ; CURRENT APPLICATION NUMBER: US/09/068,101
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: EP 96202446.9

EARLIER FILING DATE: 1996-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 10
LENGTH: 5611
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "plasmid pLH48"
FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((39)..(317))
OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
OTHER INFORMATION: T-DNA"
FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((318)..(869))
OTHER INFORMATION: label = bar, "region coding for phosphinothricin
OTHER INFORMATION: acetyl transferase"
FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((870)..(1702))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
FEATURE:
NAME/KEY: misc feature
LOCATION: (1740)..(2284)
OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum"
FEATURE:
NAME/KEY: misc feature
LOCATION: (2285)..(2560)
OTHER INFORMATION: label = synb*, "improved barstar DNA"
FEATURE:
NAME/KEY: misc feature
LOCATION: (2561)..(2892)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
US-09-068-101-10

Query Match 100.0%; Score 102; DB 4; Length 5611;
Best Local Similarity 100.0%; Pred. No. 4.6e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 60
|||
Db 3200 CTGCTTTTATCTAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 3141
QY 61 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTC 102
|||
Db 3140 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTC 3099

RESULT 12
US-08-021-667A-18
Sequence 18, Application US/08021667A
Patent No. 5434049
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0380
TELEFAX: 202-828-0380
TELEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-021-667A-18
Query Match 98.4%; Score 100.4; DB 1; Length 201;
Best Local Similarity 99.0%; Pred. No. 8.1e-20;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 60
|||
Db 43 CAGCTTTTATCTAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 102
QY 61 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTC 102
|||
Db 103 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTC 144
RESULT 13
US-08-410-544-18
Sequence 18, Application US/08410544
Patent No. 5607646
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-728-785A-18

Query Match      98.4%; Score 100.4; DB 1; Length 201;
Best Local Similarity 99.0%; Pred. No. 8.1e-20;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTTTTATACTAAGTTGGCATTATAAAAAGCATTCGTTATCAATTGTTGCAACG 60
Db      43 CAGCTTTTATACTAAGTTGGCATTATAAAAAGCATTCGTTATCAATTGTTGCAACG 102

QY      61 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTTGATTTC 102
Db      103 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTTGATTTC 144

RESULT 15
US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FARNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Query Match      98.4%; Score 100.4; DB 3; Length 4909;
Best Local Similarity 99.0%; Pred. No. 1.3e-19;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTTTTATACTAAGTTGGCATTATAAAAAGCATTCGTTATCAATTGTTGCAACG 60
Db      2375 CAGCTTTTATACTAAGTTGGCATTATAAAAAGCATTCGTTATCAATTGTTGCAACG 2316

```

QY 61 AACAGGTCACACTATCAGTCAAAATAAAATCATTATTGATTTC 102
2315 AACAGGTCACACTATCAGTCAAAATAAAATCATTATTGATTTC 2274
Db

Search completed: September 9, 2004, 21:21:19
Job time : 23.4903 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 ; Search time 184.482 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-4
Perfect score: 162
Sequence: 1 ttgtttacaggtcactaataa.....agctttttatactaacttg 162

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	162	100.0	162	4 AAF61420	AAF61420 E. coli a
2	160.4	99.0	243	4 AAF61418	AAF61418 Bacteriop
3	160.4	99.0	248	8 ACC85316	Acc85316 Recombina
4	160.4	99.0	282	7 ACC44676	Acc44676 Murine rD
5	160.4	99.0	282	7 ABT16636	ABT16636 Artificia
6	160.4	99.0	610	5 AAF79770	AAF79770 Bacteriop
7	160.4	99.0	1469	7 ABQ80306	Abq80306 Lambda fr
8	160.4	99.0	1469	7 ACC83020	Acc83020 Bacteriop
9	160.4	99.0	1763	2 AAC30709	Aac30709 Rat neuro
10	160.4	99.0	4346	7 ACC44716	Acc44716 Plasmid p
11	160.4	99.0	4346	7 ABT16615	ABT16615 Artificia
12	160.4	99.0	4909	2 AAT18924	Aat18924 Plasmid p
13	160.4	99.0	5641	4 AAF30800	AAF30800 Vector pl
14	160.4	99.0	5670	4 AAF30801	Aaf30801 Vector pl
15	160.4	99.0	5826	4 AAC30798	Aaf30798 Vector pl
16	160.4	99.0	6071	4 AAC30799	Aaf30799 Vector pl
17	160.4	99.0	7652	2 AAQ45682	Aaq45682 Sequencin
18	158.8	98.0	243	4 AAF61421	Aaf61421 E. coli a
19	152.4	94.1	17458	6 ABQ82142	Abq82142 Acceptor
20	152.4	94.1	17458	6 ABQ82141	Abq82141 Acceptor
21	152.4	94.1	17476	6 ABQ82141	Abq82141 Acceptor
22	152.4	94.1	17476	6 ABQ82141	Abq82141 Acceptor
23	152.4	94.1	17681	6 ABQ82143	Abq82143 Acceptor

C	24	152.4	94.1	17681	6	ABQ82143	Abq82143 Acceptor
C	25	150.8	93.1	4204	3	AAC55522	Aac55522 Donor pla
C	26	150.8	93.1	4208	3	AAC55523	Aac55523 Donor pla
C	27	150.8	93.1	4470	3	AAC55521	Aac55521 Donor pla
C	28	150.8	93.1	4470	7	ABZ58767	Abz58767 Destinati
C	29	150.8	93.1	4892	8	ADA50329	Ada50329 Plasmid v
C	30	150.8	93.1	4939	3	AAC55525	Aac55525 Donor pla
C	31	150.8	93.1	5584	3	AAC55632	Aac55632 Donor pla
C	32	150.8	93.1	5584	7	ABZ58766	Abz58766 Donor pla
C	33	150.8	93.1	18691	6	ABQ82130	Abq82130 Acceptor
C	34	150.8	93.1	18691	6	ABQ82130	Abq82130 Acceptor
C	35	150.6	93.0	233	3	AAC55382	Aac55382 Recombina
C	36	150.6	93.0	233	7	ACC59568	Acc59568 Nucleic a
C	37	149.2	92.1	4165	3	AAC55524	Aac55524 Donor pla
C	38	149.2	92.1	4204	3	AAC55522	Aac55522 Donor pla
C	39	149.2	92.1	4208	3	AAC55523	Aac55523 Donor pla
C	40	149.2	92.1	4428	7	ABZ58768	Abz58768 Destinati
C	41	149.2	92.1	4470	3	AAC55521	Aac55521 Donor pla
C	42	149.2	92.1	4470	7	ABZ58767	Abz58767 Destinati
C	43	149.2	92.1	4627	7	ABZ58769	Abz58769 Destinati
C	44	149.2	92.1	4627	7	ABZ58770	Abz58770 Destinati
C	45	149.2	92.1	4892	8	ADA50329	Ada50329 Plasmid v

ALIGNMENTS

RESULT 1
AAF61420
ID AAF61420 standard; DNA; 162 BP.
XX
AC AAF61420;
XX
DT 05-JUN-2001 (first entry)
XX
DE E. coli attr DNA fragment.
XX
KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
KW targeted integration; attr; ds.
XX
OS Escherichia coli.
XX
PN DE19941186-A1.
XX
PD 01-MAR-2001.
XX
PF 30-AUG-1999; 99DE-01041186.
XX
PR 30-AUG-1999; 99DE-01041186.
XX
PA (DROE/) DROEGE P.
XX
PI Droege P;
XX
DR WPI; 2001-246016/26.
XX
PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
PT for somatic cell gene therapy, uses an integrase to effect recombination
PT between att sites.
XX
PS Claim 3; Page 14; 24pp; German.
XX
CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (i) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC (III), containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences

SQ Sequence 162 BP; 43 A; 22 C; 22 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 162; DB 4; Length 162;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 60
 |||||
 Db 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 60
 |||||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 |||||
 Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 Db 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||

RESULT 2
 AAF61418
 ID AAF61418 standard; DNA; 243 BP.
 XX
 AC AAF61418;
 XX
 DT 05-JUN-2001 (first entry)
 XX
 DE Bacteriophage lambda attP DNA fragment.
 XX
 KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
 KW targeted integration; attP; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN DE19941186-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 30-AUG-1999; 99DE-01041186.
 XX
 PR 30-AUG-1999; 99DE-01041186.
 XX
 PA (DROE/) DROEGE P.
 XX
 PI Droegge P;
 XX
 DR WPI; 2001-246016/26.
 XX
 CC Sequence-specific recombination of DNA in eukaryotes, useful particularly
 CC for somatic cell gene therapy, uses an integrase to effect recombination
 CC between att sites.
 CC
 PS Claim 2; Page 13; 24pp; German.
 XX
 CC This invention describes a novel sequence-specific recombination (SSR) of
 CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
 CC II) into a cell, using an integrase (Int) to effect SSR. The invention
 CC also describes (1) a nucleic acid comprising a 243 base pair sequence
 CC (III), fully defined in the specification, or its derivatives; and (2)
 CC vector containing (III), or its derivatives, plus a therapeutic gene, or
 CC its derivatives. The method is particularly used in somatic gene therapy
 CC in humans and animals, but can be applied more generally for gene
 CC transfer to animal or plant cells. The method is simple and controllable,
 CC and provides stable and targeted integration of selected DNA sequences
 CC

SQ Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 243;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 60
 |||||
 Db 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 60
 |||||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 |||||
 Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 Db 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||

RESULT 3
 ACC85316
 ID ACC85316 standard; DNA; 248 BP.
 XX
 AC ACC85316;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE Recombinase lambda integrase attP DNA recognition sequence.
 XX
 KW Vegetable plastid transformation; transgenic; recognition sequence;
 KW plant; site-specific integration; nutrition; seed production;
 KW chemical production; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003054201-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 16-DEC-2002; 2002WO-EP014303.
 XX
 PR 20-DEC-2001; 2001DE-01063159.
 XX
 PA (SUNG-) SUNGENE GMBH & CO KGAA.
 XX
 PI Biesgen C;
 XX
 DR WPI; 2003-541820/51.
 XX
 CC Site-specific integration of DNA into plastid DNA, useful for making
 CC transgenic plants used e.g. as food, by recombinase-mediated insertion.
 CC
 PS Disclosure; Page 35; 164pp; German.
 XX
 CC The present invention relates to a method for the site-specific
 CC integration of a DNA sequence into the plastid DNA of a plant or its
 CC derived cells. Transgenic plants in which a DNA sequence has been
 CC integrated, also their cell cultures, organs, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a recognition sequence shown in the exemplification
 CC of the invention
 CC

SQ Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 8; Length 248;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 60
 |||||
 Db 6 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTCACTGTCATATGTTGTG 65
 |||||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 |||||
 Db 66 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 125
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 Db 126 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 167
 |||||

RESULT 4
ACCA4676
ID ACC44676 standard; DNA; 282 BP.
XX
XX ACC44676;
AC
XX
XX
DT 29-MAY-2003 (first entry)
XX
DE Murine rDNA PCR primer SEQ ID NO:72.
XX
XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; Aces; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; gene; ds.
XX
XX Mus musculus.
OS Synthetic.
XX
XX
XX WO200297059-A2.
XX
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017452.
XX
XX 30-MAY-2001; 2001US-0294758P.
PR 21-MAR-2002; 2002US-0366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
XX interest.
XX
XX Example 2; Page 207; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (Aces) (ii) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an Aces. (ii) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (ii) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (ii) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of Aces comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
SQ
Query Match 99.0%; Score 160.4; DB 7; Length 282;
Best Local Similarity 99.4%; Pred. No. 9.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGTCTACTAATACCATCTAGTAGTTGATTCATGATGATGATGTTGTG 60
DB 15 TCTGTTACAGTCTACTAATACCATCTAGTAGTTGATTCATGATGATGATGTTGTG 74
QY 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTA 120

DB 75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTA 134
QY 121 TATCAATTTACGTTTCTCGTTTCAGCTTTTTTATATACTAACTTG 162
DB 135 TATCAATTTACGTTTCTCGTTTCAGCTTTTTTATATACTAACTTG 176
RESULT 5
ABTI16636
ID ABTI16636 standard; DNA; 282 BP.
XX
XX ABTI16636;
AC
XX 03-APR-2003 (first entry)
DT
XX Artificial plant chromosome related oligo SEQ ID No 48.
XX
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
ds.
XX
XX Unidentified.
OS
XX WO200296923-A1.
PN
XX 05-DEC-2002.
PD
XX
XX 30-MAY-2002; 2002WO-US017451.
PF
XX
XX 30-MAY-2001; 2001US-0294687P.
PR
XX 04-JUN-2001; 2001US-0296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
PI
XX WPI; 2003-140436/13.
DR
XX
XX Producing artificial chromosome by introducing a nucleic acid into plant
PT cell, selecting artificial chromosome that has one or more repeat regions
PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX
XX Disclosure; Page 263-264; 269pp; English.
XX
XX The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention
XX
SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
Query Match 99.0%; Score 160.4; DB 7; Length 282;
Best Local Similarity 99.4%; Pred. No. 9.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db |||||
 QY 15 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 74
 Db |||||
 QY 61 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
 Db |||||
 QY 75 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 134
 Db |||||
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATTAATTAATGTTG 162
 Db |||||
 QY 135 TATCATTTTACGTTTCTCGTTCAGCTTTTATATTAATGTTG 176
 Db |||||

RESULT 6
 AAF79770
 ID AAF79770 standard; DNA; 610 BP.
 XX AC
 XX AAF79770;
 XX XX
 DT 29-MAY-2001 (first entry)
 XX XX
 DE Bacteriophage lambda attachment P region.
 XX XX
 KW Attachment P region; attP; recombination; marker gene removal; ds.
 XX XX
 OS Bacteriophage lambda.
 XX XX
 PN WO200121780-A2.
 XX XX
 PD 29-MAR-2001.
 XX XX
 PF 15-SEP-2000; 2000WO-CB003543.
 XX XX
 PR 17-SEP-1999; 99GB-00021937.
 XX XX
 PA (UYLE-) UNIV LEEDS.
 XX XX
 PI Meyer P, Zubko B;
 XX XX
 DR WPI; 2001-266072/27.
 XX XX

Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
 XX XX
 PS Claim 8; Fig 3D; 25pp; English.
 XX XX
 CC The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibiotic resistance. The present sequence is the attP coding region
 XX XX
 SQ Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 5; Length 610;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db |||||
 QY 139 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 198
 Db |||||
 QY 61 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
 Db |||||
 QY 139 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 258
 Db |||||
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATTAATTAATGTTG 162
 Db |||||
 QY 259 TATCATTTTACGTTTCTCGTTCAGCTTTTATATTAATTAATGTTG 300
 Db |||||

RESULT 7
 ABQ80306
 ID ABQ80306 standard; DNA; 1469 BP.
 XX AC
 XX ABQ80306;
 XX XX
 DT 27-JUN-2003 (first entry)
 XX XX
 DE Lambda fragment in plasmid DNA.
 XX XX
 KW Primer; PCR; amplify; lambda phage; printer material; insertion; SNP;
 XX XX
 OS deletion; single nucleotide polymorphism; sequencing; diagnosis; ss.
 XX XX
 PN WO2003027991-A1.
 XX XX
 PD 03-APR-2003.
 XX XX
 PF 24-SEP-2002; 2002WO-JP009766.
 XX XX
 PR 25-SEP-2001; 2001JP-00291249.
 XX XX
 PA (DNAP-) DNAFORM KK.
 XX XX
 PA (RIKE) RIKEN KK.
 XX XX
 PI Hayashizaki Y;
 XX XX
 DR WPI; 2003-354676/33.
 XX XX
 PT Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer applied on it.
 XX XX
 PS Example 1; Page 31-32; 91pp; English.
 XX XX

The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 bp portion of lambda phage DNA contained in a plasmid. The amplified sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or polymer applied on it. The printed material is useful in a method for synthesising DNA where the product of amplification and/or ligation is cDNA and/or full-length cDNA which is recovered and used for determination of nucleotide insertion/deletion, single nucleotide polymorphism (SNP) and sequencing analysis, in a diagnostic method for determination of nucleotide insertion/deletion, or SNP analysis. Optionally, the cDNA and/or full-length cDNA is useful for the peptide, polypeptide or protein expression. The printed material is useful in research applications, or for providing scientists with oligomer and/or polymers from the printed materials easily and immediately. From the printed material, at least an oligomer and/or polymer can be obtained immediately and directly, without need to make a request for it. The oligomers and/or polymers can be delivered and stored easily with reduced labour and time while eliminating the need to use special equipment or facilities. Thus, the printed material is a quick, efficient and inexpensive sample delivery system

Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 Query Match 99.0%; Score 160.4; DB 7; Length 1469;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db |||||
 QY 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 867
 Db |||||
 QY 61 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
 Db |||||
 QY 968 TTTTACAGTATTATGTCGTCTGTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 927
 Db |||||

QY 121 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 162
 DE ||||||||||||||||||||||||||||||||||||||||||||
 XX 928 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 969

RESULT 8
 ACC83020
 ID ACC83020 standard; DNA; 1469 BP.
 XX
 AC ACC83020;
 XX
 DT 27-AUG-2003 (first entry)
 DE Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
 XX
 KW Oligomer storage; oligomer delivery; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO2003040360-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-JP011492.
 XX
 PR 05-NOV-2001; 2001JP-00339217.
 XX
 PA (RIKE) RIKEN KK.
 XX
 PA (DNAF-) DNAFORM KK.
 XX
 PA (HAYA/) HAYASHIZAKI Y.
 XX
 PI Hayashizaki Y;
 XX
 XX WPI; 2003-441569/41.
 XX
 DR New support useful for storing and/or delivering an oligomer and/or
 PT polymer applied on support, has oligomer and/or polymer applied on it,
 PT and a loose-leaf sheet or a card.
 XX
 XX Example 1; Page 30-31; 70pp; English.
 XX
 CC The invention relates to a method for storing and/or delivering an
 CC oligomer and/or polymer applied on support. The support has oligomer
 CC and/or polymer applied on it, and is in the form of loose-leaf sheet or a
 CC card. The support is useful for storing and/or delivering an oligomer
 CC and/or polymer applied on it. The present sequence is Bacteriophage
 CC lambda DNA used in the exemplification of the invention
 XX
 SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 Query Match 99.0%; Score 160.4; DB 7; Length 1469;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTTCACCTAATACCATCTAAGTAGTTGATTCATAGTGCATGATGTTGTG 60
 Db 808 TCTGTTACAGTTCACCTAATACCATCTAAGTAGTTGATTCATAGTGCATGATGTTGTG 867

QY 61 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
 Db 868 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 927

QY 121 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 162
 Db 928 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 969

RESULT 9
 AAZ30709/c
 ID AAZ30709 standard; cDNA; 1763 BP.
 XX
 AC AAZ30709;
 XX

DT 05-JAN-2000 (first entry)
 XX Rat neuronal immediate early gene cDNA clone R280.
 DE
 XX
 KW Immediate early gene; IEG; neuron; brain; function; growth factor;
 KW transcription factor; signal transduction; cytoskeletal protein;
 KW metabolic enzyme; learning; memory; synaptic transmission; tolerance;
 KW neuronal plasticity; ds.
 XX
 OS Rattus sp.
 XX
 PN WO9940225-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US002462.
 XX
 PR 03-FEB-1998; 98US-0074135P.
 PR 12-FEB-1998; 98US-0074518P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA (BADI) BASF-LYNX BIOSCIENCE AG.
 XX
 XX Worley PF, Lanahan A, Goetz B, Hiemisch H, Kuner R, Scheek S;
 PI Nikolich K, Zhukovski E;
 XX
 DR WPI; 1999-590697/50.
 XX
 XX Novel genes and polypeptides, useful for treating conditions related to a
 PT deficiency in nIEG responsiveness to a stimulus.
 XX
 XX Claim 1; Page 114-115; 134pp; English.
 XX
 CC This sequence represents rat neuronal immediate early gene (IEG) cDNA
 CC clone R280. An IEG is a gene whose expression is rapidly increased
 CC immediately following a stimulus e.g., neuronal stimulation. Such
 CC neuronal IEGs have been found to encode a variety of proteins, including
 CC transcription factors, cytoskeletal proteins, growth factors and
 CC metabolic enzymes, as well as proteins involved in signal transduction.
 CC The identification of neuronal IEGs and the proteins they encode may
 CC provide important information about the function of neurons in, for
 CC example, learning, memory, synaptic transmission, tolerance and neuronal
 CC plasticity. Neuronal IEGs, neuronal IEG protein products, cells
 CC expressing neuronal IEGs and antibodies against neuronal IEG proteins can
 CC be used to treat an animal with a deficiency in neuronal IEG responsiveness
 CC to stimuli, such that the effect of the deficiency is minimised. The
 CC deficiency may be a reduced or elevated level of expression of an IEG.
 CC The neuronal stimulus comprises a maximal electroconvulsive seizure and
 CC its effects influence learning or memory. The IEGs and protein products
 CC are useful in identifying compounds that modulate the expression or
 CC activity of IEG nucleic acids or proteins, respectively
 XX
 SQ Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
 Query Match 99.0%; Score 160.4; DB 2; Length 1763;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTTCACCTAATACCATCTAAGTAGTTGATTCATAGTGCATGATGTTGTG 60
 Db 431 TCTGTTACAGTTCACCTAATACCATCTAAGTAGTTGATTCATAGTGCATGATGTTGTG 372

QY 61 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATGATATTTA 120
 Db 371 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATGATATTTA 312

QY 121 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 162
 Db 311 TATCATTTTACGTTTCTCGTTACGTTTCTTTTATCTAAGTTG 270

RESULT 10
 ACC44716

Db	4190	TATCATTTTACGTTTCTCGTTTCAGCTTTTATATACTAGTTG	4231
RESULT 11			
ABT16615			
ID	ABT16615	standard; DNA; 4346 BP.	
XX	AC		
XX	ABT16615;		
XX	XX		
DT	03-APR-2003	(first entry)	
XX	XX		
DE	Artificial plant chromosome related plasmid DNA SEQ ID N		
XX	XX		
KW	Plant artificial chromosome; PAC; transgenic plant; vacc		
KW	blood factor; herbicide; stress; agronomical; nutrient q		
KW	bacterial artificial chromosome; BAC; yeast artificial c		
KW	ds.		
XX	XX		
OS	Unidentified.		
XX	XX		
FN	WO200296923-A1.		
XX	XX		
PD	05-DEC-2002.		
XX	XX		
PF	30-MAY-2002; 2002WO-US017451.		
XX	XX		
PR	30-MAY-2001; 2001US-0294687P.		
PR	04-JUN-2001; 2001US-0296329P.		
XX	XX		
PA	(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.		
PA	(AGRI-) AGRISOMA INC.		
XX	XX		
FI	Perez C, Fabijanski SP, Perkins E;		
XX	XX		
DR	WPI; 2003-140436/13.		
XX	XX		
PT	Producing artificial chromosome by introducing a nucleic		
PT	cell, selecting artificial chromosome that has one or mor		
PT	with equivalent amounts of euchromatic and heterochromat		
XX	XX		
PS	Example 19; Page 255-256; 269pp; English.		
XX	XX		
CC	The invention relates to a novel method for producing pla		
CC	chromosomes. The invention also relates to methods for th		
CC	insertion of heterologous DNA into plant artificial chro		
CC	for delivery of plant chromosomes to selected cells and		
CC	isolated plant artificial chromosome (PAC) is useful for		
CC	transgenic plant, which involves introducing the PAC into		
CC	The PAC comprises a heterologous nucleic acid encoding a		
CC	such as enzymes, antisense RNA, rRNA, rDNA, structural p		
CC	proteins, ligands, receptors, ribozymes, therapeutic pro		
CC	biopharmaceutical proteins, vaccines, blood factors, ant		
CC	cytokines, growth factors, antibodies, or a product that		
CC	resistance to diseases, insects, herbicides, or stress in		
CC	heterologous nucleic acid optionally encodes a product th		
CC	agronomically important trait in the plant, e.g. a produ		
CC	nutrient use and/or improves the nutrient quality of the		
CC	heterologous nucleic acid is contained within a bacteria		
CC	chromosome (BAC) or a yeast artificial chromosome (YAC).		
CC	polynucleotide sequence represents the DNA of a plasmid		
CC	method of the invention		
XX	XX		
SQ	Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0		
Query Match	99.0%;	Score 160.4;	DB 7; Length
Best Local Similarity	99.4%;	Pred. No. 9.2e-25;	
Matches 161;	Conservative 0;	Mismatches 1;	Indels
QY	1	TCTGTTACAGGTCACTAATACCATCTTAAGTATTGATTTCATAGTACG	
Db	4070	TCTGTTACAGGTCACTAATACCATCTTAAGTATTGATTTCATAGTACG	

QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 120
XX |||||
Db 4130 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 4189
|||
QY 121 TATCATTTTACGTTTCTCGTTTCAGTTTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 162
XX |||||
Db 4190 TATCATTTTACGTTTCTCGTTTCAGTTTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 4231
|||
RESULT 12
AAT18924/c
ID AAT18924 standard; DNA; 4909 BP.
XX
AC AAT18924;
XX
DT 17-JAN-1997 (first entry)
XX
DE Plasmid pA126i.
XX
KW Spider; dragline protein; variant; monomer; polymer; circular;
KW fibre forming region; Spidroin 1; Nephila clavipes; Dp1; mimic;
KW DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope;
KW surgical suture; implant; reinforcement; film; coating; ss.
XX
OS Synthetic.
XX
FN WO9429450-A2.
XX
PD 22-DEC-1994.
XX
PF 15-JUN-1994; 94WO-US006689.
XX
PR 15-JUN-1993; 93US-00077600.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Fahnstock SR;
XX
DR WPI; 1995-036479/05.
XX
PT New synthetic variants of spider dragline protein - for making fibres
PT useful as clothing, surgical silk, plastic reinforcement etc., also
PT related DNA, vectors and transformed cells.
XX
PS Example 1; Fig 13; 168pp; English.
XX
CC This sequence represents the complete nucleotide sequence of the plasmid
CC pA126i. This plasmid was used in the construction of the vector pP510
CC which was used to express synthetic spider dragline variants, DP-1A.9 and
CC DP-1B.9. pA126i comprises a replication origin active in E. coli, a
CC selectable genetic marker which is a gene conferring resistance to
CC ampicillin, sites for the restriction endonucleases BamHI and BglII with
CC no essential sequences between them, and a third restriction site for
CC PstI, located within the selectable marker which produces cohesive ends
CC incompatible with those produced by BamHI and BglII. The polypeptide
CC monomers are variants based on a consensus sequence derived from the
CC fibre forming regions of spider dragline protein, esp. the natural
CC protein 1 (Spidroin 1) from Nephila clavipes. Synthetic analogues of Dp1
CC were designed to mimic the repeating consensus sequence of the natural
CC protein and the pattern of variation among individual repeats. DP-1A
CC analogues are composed of a tandemly repeated 101 amino acid monomer
CC which comprises four repeats which differ from the consensus sequence
CC given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine
CC sequence varies in length from 0-7 residues; (2) when the entire poly-
CC alanine sequence is deleted, so also is the surrounding sequence
CC encompassing AGRGGLGGGAGAGAGG; (3) aside from the poly-alanine sequence,
CC deletions usually encompass integral multiples of three consecutive
CC residues; (4) deletion of GYG is generally accompanied by deletion of GRG
CC in the same sequence; and (5) a repeat in which the entire poly-alanine
CC sequence is deleted is generally preceded by a repeat containing six
CC alanine residues. The proteins may be used to produce fibres of high
CC tensile strength and elasticity, suitable for clothing, rope, surgical
CC sutures, biomaterials for implants, plastic reinforcements, films,

CC coatings, etc
XX
SQ Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
Query Match 99.0%; Score 160.4; DB 2; Length 4909;
Best Local Similarity 99.4%; Pred. No. 9.2e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCACTGATATGTTGTG 60
|||
Db 2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCACTGATATGTTGTG 2457
|||
QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
|||
Db 2456 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 2397
|||
QY 121 TATCATTTTACGTTTCTCGTTTCAGTTTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 162
|||
Db 2396 TATCATTTTACGTTTCTCGTTTCAGTTTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 2355
|||
RESULT 13
AAF30800
ID AAF30800 standard; DNA; 5641 BP.
XX
AC AAF30800;
XX
DT 11-SEP-2003 (revised)
DT 21-JUN-2001 (first entry)
XX
DE Vector plasmid pJMF3 encoding LacZ-chitobiase fusion.
XX
KW Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
XX
OS Escherichia coli.
OS Vibrio harveyi.
OS Bacteriophage lambda.
OS Chimeric.
XX
Key Location/Qualifiers
FT protein_bind 1783..1810 /*tag= a
FT /*note= "CAP-cAMP binding site"
FT -35_signal 1820..1826 /*tag= b
FT /*function= "Lac promoter"
FT -10_signal 1845..1850 /*tag= c
FT /*function= "Lac promoter"
FT protein_bind 1857..1883 /*tag= d
FT /*note= "Lac repressor binding site"
FT CDS 1895..2014 /*tag= e
FT /*partial
FT /*product= "lacZ-chitobiase fusion"
XX
WO200127322-A2.
XX
PN 19-APR-2001.
XX
XX 02-AUG-2000; 2000WO-US021048.
XX
PR 13-OCT-1999; 99US-0159221P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Zyskind J;
XX
DR WPI; 2001-290731/30.
DR P-PSDB; AAB20484.
XX
PT Identifying a regulatory element capable of directing or regulating

FT transcription (e.g. a promoter) comprises providing a construct linked to
 PT a nucleic acid encoding a cytoplasmic form of chitobiase.

XX Example 1; Page 32-34; 44pp; English.

XX The present sequence is that of vector plasmid pJMF3, which includes
 CC phage lambda attP and the lac promoter with the first 21 amino acids of
 CC lacZ-alpha (from plasmid pUC19) fused in-frame to the *Vibrio harveyi*
 CC chitobiase gene (see AAB20484). The invention relates to genetic
 CC constructs and methods of using a cytoplasmic form of chitobiase enzyme
 CC as a reporter. A claimed reporter gene construct comprises pJMF3. The
 CC invention also comprises expression vectors which express the cytoplasmic
 CC form of chitobiase. Methods are provided for: characterizing a promoter;
 CC identifying a regulatory element capable of directing and regulating
 CC transcription within a test sequence; detecting a successful
 CC transformation; and for monitoring the activity of a promoter. Chitobiase
 CC has an advantage over beta-galactosidase as a reporter gene in that it is
 CC not necessary to engineer many host cells to lack reporter activity.
 CC (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 5641;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTGCATATGTTGG 60

DB 4703 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTGCATATGTTGG 4762

QY 61 TTTTACAGTATTATGTCGCTCTTTTATGCAAAATCTAATTATATATTGATATTTA 120

DB 4763 TTTTACAGTATTATGTCGCTCTTTTATGCAAAATCTAATTATATATTGATATTTA 4822

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162

DB 4823 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 4864

RESULT 14

AAAF30801/c
 ID AAF30801 standard; DNA; 5670 BP.

AC AAF30801;

XX 11-SEP-2003 (revised)

DT 21-JUN-2001 (first entry)

XX Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.

DE Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.

XX *Escherichia coli*.

OS *Vibrio harveyi*.

OS Bacteriophage lambda.

OS Chimeric.

XX Key Location/Qualifiers

FT protein_bind 1783..1810

FT /*tag= a

FT /note= "CAP-cAMP binding site"

FT -35_signal 1820..1826

FT /*tag= b

FT /function= "Lac promoter"

FT -10_signal 1845..1850

FT /*tag= c

FT /function= "Lac promoter"

FT protein_bind 1857..1883

FT /*tag= d

FT /note= "Lac repressor binding site"

FT CDS 1895..2014

FT /*tag= e

FT /partial

/product= "lacZ-chitobiase fusion"

WO200127322-A2.

19-APR-2001.

02-AUG-2000; 2000WO-US021048.

13-OCT-1999; 99US-0159221P.

(ELIT-) ELITRA PHARM INC.

Zyskind J;

WPI; 2001-290731/30.

P-PSDB; AAB20484.

Identifying a regulatory element capable of directing or regulating
 transcription (e.g. a promoter) comprises providing a construct linked to
 a nucleic acid encoding a cytoplasmic form of chitobiase.

Example 1; Page 34-36; 44pp; English.

The present sequence is that of vector plasmid pJMF4, which includes
 phage lambda attP and the lac promoter with the first 21 amino acids of
 lacZ-alpha (from plasmid pUC19) fused in-frame to the *Vibrio harveyi*
 chitobiase gene (see AAB20484). The invention relates to genetic
 constructs and methods of using a cytoplasmic form of chitobiase enzyme
 as a reporter. A claimed reporter gene construct comprises pJMF4. The
 invention also comprises expression vectors which express the cytoplasmic
 form of chitobiase. Methods are provided for: characterizing a promoter;
 CC identifying a regulatory element capable of directing and regulating
 CC transcription within a test sequence; detecting a successful
 CC transformation; and for monitoring the activity of a promoter. Chitobiase
 CC has an advantage over beta-galactosidase as a reporter gene in that it is
 CC not necessary to engineer many host cells to lack reporter activity.
 CC (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 5670;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTGCATATGTTGG 60

DB 5041 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTGCATATGTTGG 4982

QY 61 TTTTACAGTATTATGTCGCTCTTTTATGCAAAATCTAATTATATATTGATATTTA 120

DB 4981 TTTTACAGTATTATGTCGCTCTTTTATGCAAAATCTAATTATATATTGATATTTA 4922

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162

DB 4921 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 4880

RESULT 15

AAAF30798

ID AAF30798 standard; DNA; 5826 BP.

XX AAF30798;

DT 11-SEP-2003 (revised)

DT 21-JUN-2001 (first entry)

DE Vector plasmid pJMK6 encoding chitobiase reporter enzyme.

XX Chitobiase; reporter gene; dnaA gene; promoter; vector; pJMK6; ds.

XX *Escherichia coli*.

OS *Vibrio harveyi*.

OS Chimeric.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 128.856 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-3

Perfect score: 102

Sequence: 1 ctgctttttatactaagtt.....taaaatcattttgatttc 102

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	102	17	US-10-310-695-15
2	102	100.0	105	17	US-10-627-711-9
3	102	100.0	108	13	US-10-403-232-174
4	102	100.0	3049	13	US-10-432-148-4
5	102	100.0	5349	9	US-09-970-921-7
6	102	100.0	5611	9	US-09-970-921-10
7	100.4	98.4	243	13	US-10-403-232-173
8	100.4	98.4	243	17	US-10-310-695-2
9	100.4	98.4	243	17	US-10-310-695-14
10	100.4	98.4	248	17	US-10-627-711-8
11	100.4	98.4	282	15	US-10-161-403-72
12	100.4	98.4	1763	11	US-09-244-805-57
13	100.4	98.4	1763	11	US-09-245-277-57
14	100.4	98.4	1763	17	US-10-792-481-57
15	102	100.0	102	17	US-10-310-695-15
16	102	100.0	105	17	US-10-627-711-9
17	102	100.0	108	13	US-10-403-232-174
18	102	100.0	3049	13	US-10-432-148-4
19	102	100.0	5349	9	US-09-970-921-7
20	102	100.0	5611	9	US-09-970-921-10
21	100.4	98.4	243	13	US-10-403-232-173
22	100.4	98.4	243	17	US-10-310-695-2
23	100.4	98.4	243	17	US-10-310-695-14
24	100.4	98.4	248	17	US-10-627-711-8
25	100.4	98.4	282	15	US-10-161-403-72
26	100.4	98.4	1763	11	US-09-244-805-57
27	100.4	98.4	1763	11	US-09-245-277-57
28	100.4	98.4	1763	17	US-10-792-481-57

15	100.4	98.4	2959	13	US-10-270-176-8	Sequence 8, Appli
16	100.4	98.4	3663	13	US-10-270-176-3	Sequence 3, Appli
17	100.4	98.4	3695	13	US-10-270-176-13	Sequence 13, Appl
18	100.4	98.4	4346	15	US-10-161-403-113	Sequence 113, App
19	100.4	98.4	4782	13	US-10-270-176-20	Sequence 20, Appl
20	100.4	98.4	5646	13	US-10-270-176-39	Sequence 39, Appl
21	100.4	98.4	5646	13	US-10-270-176-41	Sequence 41, Appl
22	100.4	98.4	5706	13	US-10-270-176-40	Sequence 40, Appl
23	100.4	98.4	5739	13	US-10-270-176-9	Sequence 9, Appli
24	100.4	98.4	5771	13	US-10-270-176-34	Sequence 34, Appl
25	100.4	98.4	5771	13	US-10-270-176-35	Sequence 35, Appl
26	100.4	98.4	5814	13	US-10-270-176-37	Sequence 37, Appl
27	100.4	98.4	5911	13	US-10-270-176-42	Sequence 42, Appl
28	100.4	98.4	5929	13	US-10-270-176-45	Sequence 45, Appl
29	100.4	98.4	5929	13	US-10-270-176-46	Sequence 46, Appl
30	100.4	98.4	5948	13	US-10-270-176-21	Sequence 21, Appl
31	100.4	98.4	5986	13	US-10-270-176-36	Sequence 36, Appl
32	100.4	98.4	6200	13	US-10-270-176-38	Sequence 38, Appl
33	100.4	98.4	6664	13	US-10-270-176-1	Sequence 1, Appli
34	100.4	98.4	6668	13	US-10-270-176-2	Sequence 2, Appli
35	100.4	98.4	6742	13	US-10-270-176-19	Sequence 19, Appl
36	100	98.0	119	10	US-09-981-803-12	Sequence 12, Appl
37	93.8	92.0	100	13	US-10-301-849A-17	Sequence 17, Appl
38	93.8	92.0	1688	16	US-10-374-780A-393	Sequence 393, App
39	93.8	92.0	2717	15	US-10-151-690-18	Sequence 18, Appl
40	92.2	90.4	100	13	US-10-403-232-180	Sequence 180, App
41	92.2	90.4	659	15	US-10-349-782-9	Sequence 9, Appli
42	92.2	90.4	2591	15	US-10-005-876A-70	Sequence 70, Appl
43	92.2	90.4	2607	15	US-10-005-876A-71	Sequence 71, Appl
44	92.2	90.4	2831	15	US-10-241-596-133	Sequence 133, App
45	92.2	90.4	3647	15	US-10-241-596-134	Sequence 134, App

ALIGNMENTS

RESULT 1

US-10-310-695-15
; Sequence 15, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:0190S
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-310-695-15

Query Match 100.0%; Score 102; DB 17; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG	60
Db	1	CTGCTTTTATCTAAGTTGGCATTATAAAAGCATTGCTTATCAATTTGTTGCAACG	60
Qy	61	AACAGGTCATCATCAGTCAAAATAAAATCATTTGTTGATTTC	102
Db	61	AACAGGTCATCATCAGTCAAAATAAAATCATTTGTTGATTTC	102

RESULT 2

US-10-627-711-9
; Sequence 9, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:

```

; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-9

Query Match      100.0%; Score 102; DB 17; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 4 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 63

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 64 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 105

RESULT 3
US-10-403-232-174
; Sequence 174, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-174

Query Match      100.0%; Score 102; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 7 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 66

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 67 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 108

RESULT 4
US-10-432-148-4
; Sequence 4, Application US/10432148
; Publication No. US20040064853A1
; GENERAL INFORMATION:
; APPLICANT: KWS SAAT AG
; TITLE OF INVENTION: tissue specific promoter
; FILE REFERENCE: tissue specific promoter 1

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; CURRENT APPLICATION NUMBER: US/10/432,148
; CURRENT FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3049
; TYPE: DNA
; ORGANISM: Beta vulgaris
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(2998)
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (2928)..(3049)
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: (2877)..(2883)
US-10-432-148-4

Query Match      100.0%; Score 102; DB 13; Length 3049;
Best Local Similarity 100.0%; Pred. No. 5.1e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 2398 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 2457

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 102
Db 2458 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTTC 2499

RESULT 5
US-09-970-921-7/c
; Sequence 7, Application US/09970921
; Patent No. US2002013845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "T-DNA of pTTS243"
; NAME/KEY: misc feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: label = RB, "T-DNA right border"
; NAME/KEY: misc feature
; LOCATION: Complement((98)..(331))
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc feature
; LOCATION: Complement((332)..(883))
; OTHER INFORMATION: label = bar, "region coding for phosphinotricin
; NAME/KEY: misc feature
; LOCATION: Complement((884)..(2258))
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"

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; NAME/KEY: misc feature
; LOCATION: (4246)..(4577)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
; NAME/KEY: misc feature
; LOCATION: Complement((5325)..(5349))
; OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7
Query Match 100.0%; Score 102; DB 9; Length 5349;
Best Local Similarity 100.0%; Pred. No. 6.2e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db 4885 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 4826

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 102
Db 4825 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 4784

RESULT 6
US-09-970-921-10/c
; Sequence 10, Application US/09970921
; Patent No. US20020133845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pLH48"
; NAME/KEY: misc feature
; LOCATION: Complement((39)..(317))
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; NAME/KEY: misc feature
; LOCATION: Complement((318)..(869))
; OTHER INFORMATION: label = bar, "region coding for phosphinotricin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc feature
; LOCATION: Complement((870)..(1702))
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc feature
; LOCATION: (1740)..(2284)
; OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum"
; NAME/KEY: misc feature
; LOCATION: (2285)..(2560)
; OTHER INFORMATION: label = synb+, "improved barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (2561)..(2892)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
US-09-970-921-10
Query Match 100.0%; Score 102; DB 9; Length 5611;
Best Local Similarity 100.0%; Pred. No. 6.3e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
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Db 3200 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 3141

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 102
Db 3140 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 3099

RESULT 7
US-10-403-232-173
; Sequence 173, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
; US-10-403-232-173
Query Match 98.4%; Score 100.4; DB 13; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 102
Db 202 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 243

RESULT 8
US-10-310-695-2
; Sequence 2, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DBEE.019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-310-695-2
Query Match 98.4%; Score 100.4; DB 17; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTTC 102
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Db 202 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 243

RESULT 9
US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEB:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

Query Match 98.4%; Score 100.4; DB 17; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 201

QY 61 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 202 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 243

RESULT 10
US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: SCREENING OF CDNA CLONES
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 98.4%; Score 100.4; DB 17; Length 248;
Best Local Similarity 99.0%; Pred. No. 6e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 147 CAGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 206

QY 61 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 207 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 248

RESULT 11
US-10-161-403-72
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```
; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp
US-10-161-403-72

Query Match 98.4%; Score 100.4; DB 15; Length 282;
Best Local Similarity 99.0%; Pred. No. 6.2e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 156 CAGCTTTTATCTAAGTTGCGATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 215

QY 61 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 216 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 257

RESULT 12
US-09-244-805-57/c
; Sequence 57, Application US/09244805
; Publication No. US20030203840A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Helmisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/074,518
; EARLIER FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,135
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1763)
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; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57

Query Match      98.4%; Score 100.4; DB 11; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 13
US-09-245-277-57/c
; Sequence 57, Application US/09245277
; Publication No. US20030211984A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: JHU1530-3
; CURRENT APPLICATION NUMBER: US/09/245,277
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57

Query Match      98.4%; Score 100.4; DB 11; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 14
US-10-792-481-57/c
; Sequence 57, Application US/10792481
; Publication No. US20040152658A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolic, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
```

```
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/10/792,481
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/244,805
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-10-792-481-57

Query Match      98.4%; Score 100.4; DB 17; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 15
US-10-270-176-8
; Sequence 8, Application US/10270176
; Publication No. US20040033609A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2959
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-8

Query Match      98.4%; Score 100.4; DB 13; Length 2959;
Best Local Similarity 99.0%; Pred. No. 1.4e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 1082 CAGCTTTTATCTAAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 1141

QY 61 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 1142 AACAGGTCACATCAGTCAAAATAAAATCAATTATTGATTTC 1183
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Search completed: September 10, 2004, 00:14:08
Job time : 129.856 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11 ; Search time 35.7198 Seconds
(without alignments)
2516.866 Million cell updates/sec

Title: US-10-082-772B-4

Perfect score: 162
Sequence: 1 tctgttacaggctcaactaata.....agcttttttatactaacttg 162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	160.4	99.0	4909	3	US-08-556-978B-78
C 2	160.4	99.0	6043	4	US-09-630-929-4
C 3	160.4	99.0	7652	1	US-07-590-988A-1
C 4	104.6	64.6	38584	4	US-09-433-702B-50
C 5	97.4	60.1	200	1	US-08-021-667A-17
C 6	97.4	60.1	200	1	US-08-410-544-17
C 7	97.4	60.1	200	1	US-08-728-785A-17
C 8	67.8	41.9	9827	4	US-09-453-702B-66
C 9	61.4	37.9	201	1	US-08-021-667A-18
C 10	61.4	37.9	201	1	US-08-410-544-18
C 11	61.4	37.9	201	1	US-08-728-785A-18
C 12	39	24.1	640681	4	US-09-730-988-1
C 13	38.2	23.6	19124	2	US-08-487-826B-13
C 14	37.6	23.2	640681	4	US-09-790-988-1
C 15	37.4	23.1	7786	4	US-09-790-988-2
C 16	37.2	23.0	3078	4	US-03-601-198-54
C 17	36.4	22.5	5455	4	US-10-204-708-33
C 18	36.4	22.5	10467	4	US-10-204-708-2
C 19	36	22.2	1725	4	US-08-882-164D-31
C 20	36	22.2	6326	4	US-10-204-708-57
C 21	36	22.2	11131	4	US-10-204-708-27
C 22	35.8	22.1	6306	4	US-10-204-708-50
C 23	35.8	22.1	786431	4	US-09-751-389-3
C 24	35.2	21.7	658	3	US-08-998-416-595
C 25	35.2	21.7	5844	4	US-10-204-708-88
C 26	35.2	21.7	6182	4	US-10-204-708-88
C 27	35	21.6	855	4	US-08-961-527-245

C 28	35	21.6	1493	1	US-08-340-820-24
C 29	35	21.6	1493	1	US-08-593-535-24
C 30	35	21.6	3452	4	US-09-576-594-856
C 31	35	21.6	11049	4	US-10-204-708-22
C 32	35	21.6	13425	4	US-08-961-527-151
C 33	35	21.6	1664976	4	US-08-916-421B-1
C 34	34.8	21.5	783	4	US-08-956-171B-834
C 35	34.8	21.5	6243	2	US-09-056-075-1
C 36	34.6	21.4	19233	4	US-10-204-708-45
C 37	34.4	21.2	1495	4	US-09-807-258-21
C 38	34.4	21.2	6072	3	US-09-535-381-3
C 39	34.2	21.1	1442	4	US-09-227-357-119
C 40	34.2	21.1	5111	4	US-09-004-838-118
C 41	34.2	21.1	6020	4	US-10-204-708-8
C 42	34.2	21.1	19513	4	US-10-204-708-39
C 43	34	21.0	732	4	US-09-134-000C-2779
C 44	34	21.0	1664976	4	US-08-916-421B-1
C 45	33.8	20.9	998	3	US-09-122-400B-5

ALIGNMENTS

RESULT 1

US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Sequence 24, Appl

Sequence 24, Appl

Sequence 856, App

Sequence 22, Appl

Sequence 151, App

Sequence 1, Appli

Sequence 834, App

Sequence 1, Appli

Sequence 45, Appl

Sequence 21, Appl

Sequence 3, Appli

Sequence 119, App

Sequence 118, App

Sequence 8, Appli

Sequence 39, Appl

Sequence 2779, Ap

Sequence 1, Appli

Sequence 5, Appli

Query Match 99.0%; Score 160.4; DB 3; Length 4909;

Best Local Similarity 99.4%; Pred. No. 1.6e-26;

Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCTGTTACAGTCTACTAATCACTAGTAGTGTGATTCATAGTACTGATGCTGATGTTGTG 60

Db 2516 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTATTTCATAGTGAATGATGTTGTG 2457
 QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
 Db 2456 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 2397
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
 Db 2396 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 2355

RESULT 2

US-09-630-929-4/c
 ; Sequence 4, Application US/09630929
 ; Patent No. 6620585
 ; GENERAL INFORMATION:
 ; APPLICANT: Judith W. Zyskind
 ; TITLE OF INVENTION: USE OF ECOTOXINS AND SECRETED ENZYMES
 ; FILE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
 ; FILE REFERENCE: ELITRA.012A
 ; CURRENT APPLICATION NUMBER: US/09/630,929
 ; CURRENT FILING DATE: 2000-08-02
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 6043
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi
 ; OTHER INFORMATION: sequences inserted
 US-09-630-929-4

Query Match 99.0%; Score 160.4; DB 4; Length 6043;
 Best Local Similarity 99.4%; Pred. No. 1.6e-28;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTATTTCATAGTGAATGATGTTGTG 60
 Db 5414 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTATTTCATAGTGAATGATGTTGTG 5355

QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
 Db 5354 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 5295
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
 Db 5294 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 5253

RESULT 3

US-07-590-988A-1
 ; Sequence 1, Application US/07590988A
 ; Patent No. 5227288
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; TITLE OF INVENTION: DNA Sequencing Vector with
 ; TITLE OF INVENTION: Reversible Insert
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Quarles and Brady
 ; STREET: P.O. BOX 2113
 ; STREET: FIRST WISCONSIN PLAZA
 ; CITY: MADISON
 ; STATE: WISCONSIN
 ; COUNTRY: U.S.A.
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh
 ; SOFTWARE: Microsoft word 4.0
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/590,988A
 ; FILING DATE: 19901001
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nicholas J. Seay
 ; REGISTRATION NUMBER: 27,386
 ; REFERENCE/DOCKET NUMBER: 9629691682
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 251-5000
 ; TELEFAX: (608) 251-9166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7652 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: Other nucleic acid;
 ; DESCRIPTION: synthetic recombinant plasmid
 ; HYPOHETICAL: no
 ; ANTI-SENSE: no
 US-07-590-988A-1
 Query Match 99.0%; Score 160.4; DB 1; Length 7652;
 Best Local Similarity 99.4%; Pred. No. 1.6e-28;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTATTTCATAGTGAATGATGTTGTG 60
 Db 5933 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTATTTCATAGTGAATGATGTTGTG 5992
 QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
 Db 5993 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 6052
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
 Db 6053 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 6094
 RESULT 4
 US-09-453-702B-50
 ; Sequence 50, Application US/09453702B
 ; Patent No. 6365723
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; Burland, Valerie
 ; Perna, Nicole T.
 ; Plunkett, Guy
 ; Welch, Rod
 ; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Quarles & Brady
 ; STREET: 1 South Pinckney Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: US
 ; ZIP: 53701-2113
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 8.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/453,702B
 ; FILING DATE: 03-Dec-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/110,955
 ; FILING DATE: 04-DEC-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27386

```

; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38564
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-453-702B-50

Query Match 64.6%; Score 104.6; DB 4; Length 38584;
Best Local Similarity 83.2%; Pred. No. 9.9e-16;
Matches 119; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 60
Db 38442 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 38501

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATTTA 120
Db 38502 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATTTA 38561

QY 121 TATCATTTACGTTTCTCGTTCA 143
Db 38562 TGGGTTTGCTGTTTCGTTCA 38584

RESULT 5
US-08-021-667A-17
; Sequence 17, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021.667A
; FILING DATE: 19930224
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0380
; TELEFAX: 202-828-0380
; TELEX: 440280/248545
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-410-544-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 161

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 200

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; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-021-667A-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 161

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 200

RESULT 6
US-08-410-544-17
; Sequence 17, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0380
; TELEFAX: 202-828-0380
; TELEX: 248545
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-410-544-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTGTG 161

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QY 61 TTTTACAGTATTAGTCTGTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTAGTCTGTTTATGCAAAATCT 200

RESULT 7
US-08-728-785A-17
; Sequence 17, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/410,544
; FILING DATE: 21-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667

; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; Query Match 60.1%; Score 97.4; DB 1; Length 200;
; Best Local Similarity 99.0%; Pred. No. 3.1e-14;
; Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGCTGATGTTGTG 60
Db 102 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGCTGATGTTGTG 161
QY 61 TTTTACAGTATTAGTCTGTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTAGTCTGTTTATGCAAAATCT 200

RESULT 8
US-09-453-702B-66/c
; Sequence 66, Application US/09453702B

; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9827
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-453-702B-66

Query Match 41.9%; Score 67.8; DB 4; Length 9827;
Best Local Similarity 69.0%; Pred. No. 2.3e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGCTGATGTTGT- 59
Db 938 TCTGAACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGCATGCTGATGTTGTG 879
QY 60 GTTTTACAGTATTAGTCTGTTTATGCAAAATCTAATTAATATATGATATT 119
Db 878 GTCTTGAGTATTATATAGCCTATATTATGATTCAGCCATCATATCTATGATCGT 819
QY 120 ATATCATTTTACGTTTCTCGTTACGCTTTTATA 154
Db 818 AAATGGGTTTTATTGTTGGTGGTGGCGCTTTTA 784

RESULT 9
US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Antonelli, Terry, Stout & Kraus
;; STREET: Suite 600, 1919 Pennsylvania Ave., NW
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20006
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/021,667A
;; FILING DATE: 19930224
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Terry, David T.
;; REGISTRATION NUMBER: 20,178
;; REFERENCE/DOCKET NUMBER: 520.31930X00
;; TELEPHONE: 202-828-0300
;; TELEFAX: 202-828-0380
;; TELEX: 440280/248545
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 201 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;;
US-08-021-667A-18

Query Match 37.9%; Score 61.4; DB 1; Length 201;
Best Local Similarity 98.4%; Pred. No. 5.1e-06;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 100 AATTTAATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACATAAC 159
Db 1 AATTTAATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACATAAG 60
QY 160 TTG 162
Db 61 TTG 63

RESULT 10
US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544

;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/021,667
;; FILING DATE: 24-FEB-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Terry, David T.
;; REGISTRATION NUMBER: 20,178
;; REFERENCE/DOCKET NUMBER: 520.31930X00
;; TELEPHONE: 202-828-0300
;; TELEFAX: 202-828-0380
;; TELEX: 248545
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 201 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;;
US-08-410-544-18

Query Match 37.9%; Score 61.4; DB 1; Length 201;
Best Local Similarity 98.4%; Pred. No. 5.1e-06;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 100 AATTTAATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACATAAC 159
Db 1 AATTTAATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACATAAG 60
QY 160 TTG 162
Db 61 TTG 63

RESULT 11
US-08-728-785A-18
; Sequence 18, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/410,544
; FILING DATE: 21-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178

RESULT 13
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:

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RESULT 14
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF H
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-02-23

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; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match      23.2%; Score 37.6; DB 4; Length 640681;
Best Local Similarity 54.3%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 64;

QY 12 TCACTAATACCATCTAAGTAGTGTGATCATAGTGAAGTGCATATGTTGTTTACAGTAT 71
Db 451315 TCATAAAACATTTTGTGAATATAATTTTAAAGATAGATTTTCTTTTACCAC 451256

QY 72 TAGGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATATATCAATTTTAC 131
Db 451255 ATTATATTTAATTTAATAATAAATTAACCTTAATATATATATATGATACATAAT 451196

QY 132 GTTTCCTCGTTCAGCTTTTTT 151
Db 451195 GTTTTTGTGTTTAATTTTT 451176

RESULT 15
US-09-790-988-2
; Sequence 2, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7786
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-2

Query Match      23.1%; Score 37.4; DB 4; Length 7786;
Best Local Similarity 57.1%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 51;

QY 42 AGTGACTGCATATGTTGTTTACAGTATATGATGCTGTTTTTTATGCAAAATCTAA 101
Db 1219 AGTGGTTCATTTTTTATATATTTCAAAATATATAAATTTTATTTTCTTTCAATAA 1278

QY 102 TTTAATATATGATATTTATATCAATTTTACGTTTCTCGTTCAGCTTTTTTATCTAACT 160
Db 1279 TTAAATTTTTTATATTTAAGATATATACTTTCTTTTATTTTTTTTATGAAATAT 1337

Search completed: September 9, 2004, 21:21:23
Job time : 39.7198 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 ; Search time 1308.61 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-4

Perfect score: 162

Sequence: 1 tctgtacagggtcactaata.....agcttttttatactaacttg 162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	162	100.0	770	28	AQ991774
C 2	162	100.0	791	28	AQ991791
C 3	160.4	99.0	712	28	AQ990809
C 4	155.4	95.9	708	28	AQ990869

5	154	95.1	299	13	BY115594
6	150.6	93.0	827	14	CF347641
7	149.6	92.3	787	14	CF347604
8	149	92.0	755	14	CF347718
C 9	140.8	86.9	756	28	AQ991732
C 10	137.8	85.1	777	14	CF347686
C 11	134.6	83.1	583	14	CB403882
C 12	133.8	82.1	395	28	AQ991303
C 13	129.8	80.1	393	14	CB403984
C 14	128.8	79.5	764	28	AQ990470
C 15	126.2	77.9	764	28	AQ990878
C 16	123.6	76.3	487	14	CB395230
C 17	121	74.7	556	28	AQ991338
C 18	114.8	70.9	743	28	AQ990346
C 19	114.4	70.6	472	13	BQ157398
C 20	114.4	70.6	473	13	BQ156404
C 21	114.2	70.5	758	28	AQ991690
C 22	104.8	64.7	751	28	AQ989566
C 23	103	63.6	753	28	AQ990861
C 24	102.8	63.5	553	14	CF347596
C 25	94.2	58.1	746	28	AQ990173
C 26	92.2	56.9	811	14	CF347776
C 27	88.8	54.8	808	28	AQ990388
C 28	88.8	54.8	810	14	CF347481
C 29	86.8	53.6	719	28	AQ991352
C 30	81.6	50.4	715	28	AQ991358
C 31	76.8	47.4	695	28	AQ991039
C 32	76.2	47.0	384	12	B1174407
C 33	74.6	46.0	767	28	AQ990301
C 34	67.4	41.6	597	12	B1422679
C 35	67.2	41.5	800	14	CF347726
C 36	62.8	38.8	764	28	AQ990110
C 37	61.4	37.9	206	13	BQ156416
C 38	57.8	35.7	767	14	CF347722
C 39	54.8	33.8	329	9	AA386440
C 40	54.8	33.8	823	14	CF347730
C 41	50.6	31.2	675	28	AQ991241
C 42	47	29.0	609	28	AZ522574
C 43	46.8	28.9	672	28	AQ990864
C 44	46.4	28.6	591	14	CB404318
C 45	46.4	28.6	737	29	BX154196

ALIGNMENTS

RESULT 1
AQ991774/c

LOCUS

DEFINITION

AQ991774 770 bp DNA linear GSS 14-AUG-2000
RfC02039F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02039F, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AQ991774.1 GI:9650368

GSS.

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 770)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

20378633

10919786

Contact: ffrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

source
 Location/Qualifiers
 1..770
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02039F"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 162; DB 28; Length 770;
 Best Local Similarity 100.0%; Pred. No. 7.3e-22;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db 197 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 138

QY 61 TTTTACAGTATTATAGTCTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
 Db 137 TTTTACAGTATTATAGTCTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 78

QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATGATATTTA 162
 Db 77 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATGATATTTA 36

RESULT 2

AQ991791/c
 LOCUS
 DEFINITION
 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02369F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

AQ991791 791 bp DNA linear GSS 14-AUG-2000
 Rf02369F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02369F, genomic survey sequence.
 AQ991791 GI:9650395
 GSS.
 Photorhabdus luminescens
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 1 (bases 1 to 791)
 french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 10919786
 Contact: french-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk

This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

source
 Location/Qualifiers

source

1..791
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02368F"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 162; DB 28; Length 791;
 Best Local Similarity 100.0%; Pred. No. 7.2e-22;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db 194 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 135

QY 61 TTTTACAGTATTATAGTCTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
 Db 134 TTTTACAGTATTATAGTCTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 75

QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATGATATTTA 162
 Db 74 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATGATATTTA 33

RESULT 3

AQ990809/c
 LOCUS
 DEFINITION
 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01638, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

AQ990809 712 bp DNA linear GSS 14-AUG-2000
 Rf01638 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01638, genomic survey sequence.
 AQ990809 GI:9649403
 GSS.
 Photorhabdus luminescens
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 1 (bases 1 to 712)
 french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 10919786
 Contact: french-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res
 Seq primer: M13 Forward
 Class: shotgun.

FEATURES

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 Location/Qualifiers
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 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01638"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"

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Library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match          99.0%; Score 160.4; DB 28; Length 712;
Best Local Similarity 99.4%; Pred. No. 1.5e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCTAAGTAGTGAATTCATAGTGAAGTGCATATGTTG 60
    |||||
Db 591 TCTGTTACAGGTCACCTAATACCTAAGTAGTGAATTCATAGTGAAGTGCATATGTTG 532

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCGAAATCTAATTTAATATATGATATTA 120
    |||||
Db 531 TTTTACAGTATTATGAGTCTGTTTTTATGCGAAATCTAATTTAATATATGATATTA 472

QY 121 TATCATTTTACGTTCTCGTTACGCTTTTTTATCTAACTTG 162
    |||||
Db 471 TATCATTTTACGTTCTCGTTACGCTTTTTTATCTAACTTG 430

RESULT 4
AQ990869/c
LOCUS
DEFINITION
Photobacterium luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG01706, genomic survey
sequence.
ACCESSION
AQ990869
VERSION
AQ990869.1 GI:9649463
KEYWORDS
GSS.
SOURCE
Photobacterium luminescens
ORGANISM
Photobacterium luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photobacterium.
REFERENCE
1 (bases 1 to 708)
french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
MEDLINE
PUBMED
10919786
COMMENT
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1..708
/organism="Photobacterium luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01706"
/dev_stage="primary phase variant"
/clone_lib="Photobacterium luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match          95.9%; Score 155.4; DB 28; Length 708;
Best Local Similarity 99.4%; Pred. No. 1.4e-20;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 6 TACAGTCACTAATACCACTAAGTAGTGAATTCATAGTGAAGTGCATATGTTGTTT 65
    |||||
Db 481 TACAGGTCACTAATACCACTAAGTAGTGAATTCATAGTGAAGTGCATATGTTGTTT 422

QY 66 CAGTATTATGAGTCTGTTTTTATGCGAAATCTAATTTAATATGATATTAATATCA 125
    |||||
Db 421 CAGTATTATGAGTCTGTTTTTATGCGAAATCTAATTTAATATGATATTAATATCA 362

QY 126 TTTTACGTTTCTCGTTACGCTTTTTTATCTAACTTG 162
    |||||
Db 361 TTTTACGTTTCTCGTTACGCTTTTTTATCTAACTTG 325

RESULT 5
BY115594
LOCUS
DEFINITION
BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus
musculus cDNA clone L430040C03 5', mRNA sequence.
ACCESSION
BY115594
VERSION
BY115594.1 GI:26226695
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 299)
Ozaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,K.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,
Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustinch,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempie,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,I.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
MEDLINE
PUBMED
12466851
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/

```

Havashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers

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1..239
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L430040C03"
/tissue_type="whole body"
/dev_stages="18 days embryo"
/clone_lib="RIKEN full-length enriched, 18 days embryo
whole body"
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ORIGIN

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Query Match      95.1%; Score 154; DB 13; Length 299;
Best Local Similarity 96.9%; Pred. No. 3.4e-20;
Matches 157; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATATACCATCTAAGTAGTGTGATTCATAGTGACATGCTATGTTGG 60
Db 108 TCTGTCACAGGTCATATACCATCTAAGTAGTGTGATTCATAGTGACATGCTATGTTGG 167

QY 61 TTTTACAGTATTATGAGTCTCTTTTTTATGCAAAATCTAATTAATATGATTTA 120
Db 168 TTTTACAGTATTATGAGTCTCTTTTTTATGCAAAATCTAATTAATATGATTTA 227

QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATACACTTG 162
Db 228 TATCATTTTACGTTTCTCGTTACGCTTTTATACACTTG 269
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RESULT 6

CF347641

LOCUS

```
DEFINITION AGENCOURT_15225345 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001697
5', mRNA sequence.
```

ACCESSION

CF347641

VERSION

CF347641.1

GI:33790724

KEYWORDS

EST

SOURCE

Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 827)

NIH-MGC <http://mgc.nci.nih.gov/>;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

cDNA Library Preparation: Open Biosystems

FEATURES

source

1..827

Location/Qualifiers

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:7001697"

/tissue_type="whole body"

/lab_host="DH10B"

/clone_lib="NIH_ZGC_10"

/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;

Bulk tissue was collected from a whole adult individual

from the Tuebingen strain. 1st strand cDNA was primed with

a Not I - oligo(dT) primer, double-stranded cDNA was

cloned into the Not I and EcoRV sites of pExpress-1.

Library was size-selected for >1 kb fragments. A

normalized version of this library is also available

(NIH_ZGC_7). Library was constructed by Open Biosystems

(Huntsville, AL)."

ORIGIN

Query Match

Best Local Similarity

93.0%; Score 150.6; DB 14; Length 827;

Matches 153; Conservative

0; Mismatches 4; Indels

0; Gaps

0;

QY

6 TACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGACATGCTATGTTGTTTAA 65

Db

88 TACAGTCACTAATACCATCTAAGTAGTGTGTTTCAATGATGATGCTATGTTGTTTAA 147

QY

66 CAGTATTATAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTATATCA 125

Db

148 CAGTATTATAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTATATCA 207

QY

126 TTTTACGTTTCTCGTTACGCTTTTTTATACAACTTG 162

Db

208 TTTTACGTTTCTCGTTACGCTTTTTTATACAACTTG 244

RESULT 7

CF347604

LOCUS

DEFINITION

AGENCOURT_15225252 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001739

5', mRNA sequence.

ACCESSION

CF347604

VERSION

CF347604.1

GI:33790651

KEYWORDS

EST.

SOURCE

Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 787)

NIH-MGC <http://mgc.nci.nih.gov/>;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM14695 row: g column: 08
 High quality sequence start: 26
 High quality sequence stop: 468.

Location/Qualifiers
 1..827
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7001697"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_10"
 /note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments. A
 normalized version of this library is also available
 (NIH_ZGC_7). Library was constructed by Open Biosystems
 (Huntsville, AL)."

ORIGIN
 Query Match 93.0%; Score 150.6; DB 14; Length 827;
 Best Local Similarity 97.5%; Pred. No. 1.1e-19;
 Matches 153; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGACATGCTATGTTGTTTAA 65
 Db 88 TACAGTCACTAATACCATCTAAGTAGTGTGTTTCAATGATGATGCTATGTTGTTTAA 147

QY 66 CAGTATTATAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTATATCA 125
 Db 148 CAGTATTATAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTATATCA 207

QY 126 TTTTACGTTTCTCGTTACGCTTTTTTATACAACTTG 162
 Db 208 TTTTACGTTTCTCGTTACGCTTTTTTATACAACTTG 244

RESULT 7
 CF347604
 LOCUS
 DEFINITION AGENCOURT_15225252 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001739
 5', mRNA sequence.

ACCESSION
 CF347604
 VERSION
 CF347604.1
 GI:33790651
 KEYWORDS
 EST.
 SOURCE
 Danio rerio (zebrafish)
 ORGANISM
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE
 1 (bases 1 to 787)
 NIH-MGC <http://mgc.nci.nih.gov/>;
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Len Zon, Harvard
 cDNA Library Preparation: Open Biosystems
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM14695 row: i column: 02
High quality sequence stop: 698.

FEATURES

source

1. .787
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001739"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

ORIGIN

Query Match 92.3%; Score 149.6; DB 14; Length 787;
Best Local Similarity 97.4%; Pred. No. 1.7e-19; Indels 0; Gaps 0;
Matches 152; Conservative 0; Mismatches 4;

QY 6 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTCACTATGTTGGTTTAA 65
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Db 39 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTATGTTGGTTTAA 98
|||||

QY 66 CAGTATTATGATGCTCTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 125
|||||
Db 99 CAGTATTATGATGCTCTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 158
|||||

QY 126 TTTTACGTTCTCGTTCAGCTTTTATCTAAGTTG 161
|||||
Db 159 TTTTACGTTCTCGTTCAGCTTTTATCTAAGTTG 194
|||||

RESULT 8
CF347718
LOCUS CF347718 755 bp mRNA linear EST 18-AUG-2003
DEFINITION AGENCOURT15225501 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001611
5', mRNA sequence.

ACCESSION CF347718
VERSION CF347718.1 GI:33790878
KEYWORDS EST
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 755)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov

Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14695 row: c column: 18
High quality sequence stop: 184.
Location/Qualifiers
1. .755

FEATURES

source

/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001611"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

ORIGIN

Query Match 92.0%; Score 149; DB 14; Length 755;
Best Local Similarity 96.8%; Pred. No. 2.2e-19; Indels 0; Gaps 0;
Matches 152; Conservative 0; Mismatches 5;

QY 6 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTCACTATGTTGGTTTAA 65
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Db 39 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTCACTATGTTGGTTTAA 98
|||||

QY 66 CAGTATTATGATGCTCTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 125
|||||
Db 99 CAGTATTATGATGCTCTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 158
|||||

QY 126 TTTTACGTTCTCGTTCAGCTTTTATCTAAGTTG 162
|||||
Db 159 TTTTACGTTCTCGTTCAGCTTTTATCTAAGTTG 195
|||||

RESULT 9

AQ991732 756 bp DNA linear GSS 14-AUG-2000
LOCUS RfC00380F Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG00380F, genomic survey
sequence.

ACCESSION AQ991732
VERSION AQ991732.1 GI:9650228
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 756)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
JOURNAL Photorhabdus luminescens W14: potential implications for virulence
MEDLINE Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 20378633
COMMENT 10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssr@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.

FEATURES

source

1. .756
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"

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/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00380F"
/dev_stage="primary phase variant"
/clone_lib="Photorehabus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
Query Match      86.9%; Score 140.8; DB 28; Length 756;
Best Local Similarity 93.9%; Pred. No. 8.3e-18;
Matches 153; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 TCTGTTACAGTCA-CTATACACCTCAAGTCTAGTTGATTCATAGTCAGTCGATAGTCTTGT 59
Db 509 TTGTTANAGGTCACCTAATACCAATTAAGTCTAGTTGATTCATAGTCAGTCGATAGTCTTGT 450

QY 60 GTTTTACAGTATATGCTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTT 119
Db 449 GTTTTACANNANTATGCTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTT 390

QY 120 ATATCATTTTACGTTCTCGTTTCAGCTTTTATATCTAACTTG 162
Db 389 ATATCATTTTACGTTCTCGTTTCAGCTTTTATATCTAACTTG 347

RESULT 10
CF347686
LOCUS
DEFINITION
AGENCOURT_15225248 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001643
5', mRNA sequence.
ACCESSION
CF347686
VERSION
CF347686.1 GI:33790813
KEYWORDS
EST:
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 777)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bl39, 31 Rm10A07 Bethesda, MD 20892
Email: cgapps-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14695 row: e column: 02
High quality sequence start: 373
High quality sequence stop: 674.

FEATURES
Location/Qualifiers
1..777
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001643"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1."

Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

```

```

Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

ORIGIN
Query Match      85.1%; Score 137.8; DB 14; Length 777;
Best Local Similarity 92.4%; Pred. No. 3.1e-17;
Matches 145; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 6 TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCAGTCATATGTTGTGTTTAA 65
Db 39 TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCAGTCATATGTTGTGTTTAA 98

QY 66 CAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATATATCA 125
Db 99 CAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATATATCA 158

QY 126 TTTTACGTTTCTCGTTTCAGCTTTTATATCTAACTTG 162
Db 159 TTTTACGATTCTCGTTTCAGCTTTTATGACAAACTTG 195

RESULT 11
CB403882/c
LOCUS
DEFINITION
CB403882
ACCESSION
CB403882.1 GI:30745609
VERSION
EST.
KEYWORDS
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 583)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
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/strain="N2"
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subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN

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Query Match 83.1%; Score 134.6; DB 14; Length 583;
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 Matches 137; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 DB 141 TCAGTACAGGTCACATATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 82

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 120
 DB 81 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 22

QY 121 TATCATTTTACGTTCTCGTT 141
 DB 21 TATCATTTTACGTTCTCGTT 1

RESULT 12
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 LOCUS AQ991303 395 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rf02205 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02205, genomic survey
 sequence.
 ACCESSION AQ991303.1 GI:9649897
 VERSION AQ991303
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 395)
 AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826521
 Fax: (44) 1225 826779
 Email: bsr1c@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.
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 /clone="PLG02205"
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 kb) and then cloned into M13 Janus."

ORIGIN
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 Best Local Similarity 91.2%; Pred. No. 2.2e-16;
 Matches 146; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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 DB 345 TGTTCAGGTCACATAA-ACCATAATAGTAGTTNATTCATAGTACGATATGTTGTT 287

QY 63 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTATA 122
 DB 286 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTATA 227

QY 123 TCAATTTACGTTCTCGTTTCAGCTGTTTTTATGCAAAATCTAATTTAAATATGATATTTA 162
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RESULT 13
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 DEFINITION OSTR015E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB403984
 VERSION CB403984.1 GI:30745711
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 393)
 AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
 Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
 Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
 Tollas,P.P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.
 TITLE C. elegans ORFome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 JOURNAL Nat. Genet. (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
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 /note="The AD-wrmcDNA library was generated with poly(A) +
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

ORIGIN
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 Best Local Similarity 95.0%; Pred. No. 1.3e-15;
 Matches 134; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
 DB 141 TCAGTACAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 82

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 120
 DB 81 TTTCACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 22

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QY 121 TATCATTTTACGTTTCTCGTT 141
Db 21 TATCATCTCAGCTTCTCGTT 1

RESULT 14
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LOCUS
DEFINITION
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  Rfc01245 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01245, genomic survey
  sequence.
ACCESSION
  AQ990470
VERSION
  AQ990470.1 GI:9649064
KEYWORDS
  GSS.
ORGANISM
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 769)
  ffrench-Constant R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bsrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
  Location/Qualifiers
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    /note="Genomic DNA from strain W14 was size selected (1-2
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Best Local Similarity 90.7%; Pred. No. 1.6e-15;
Matches 147; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 2 CTGTTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTCACTGCATATGTTGTG 61
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QY 62 TTTCAGATTAATGATGCTGTTTTTATGCAAAATCTAATTTAATATATATTCATATTAT 121
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QY 122 ATCATTTACGTTTC-TGCTTCAGCTTTTTTATACAACTTG 162
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  764 bp DNA linear GSS 14-AUG-2000
  Rfc01715 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01715, genomic survey
  sequence.
ACCESSION
  AQ990878
VERSION
  AQ990878.1 GI:9649472
KEYWORDS
  GSS.
ORGANISM
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 764)
  ffrench-Constant R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bsrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
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ORIGIN
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Best Local Similarity 95.9%; Pred. No. 5.1e-15;
Matches 139; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 6 TACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTCACTGCATATGTTGTGTTTA 65
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QY 66 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATTCATATTATATCA 125
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QY 126 TTTACGTTTCTCGTTTCAGCTTTTT 150
Db 644 TTTACGTTTCTCGTTTCAGCTTTTT 620

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Job time : 1309.61 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 204.654 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	162	17	US-10-310-695-16
2	162	100.0	166	13	US-10-403-232-175
3	162	100.0	168	17	US-10-627-711-10
4	160.4	99.0	243	13	US-10-403-232-173
5	160.4	99.0	243	17	US-10-310-695-14
6	160.4	99.0	248	17	US-10-627-711-8
7	160.4	99.0	282	15	US-10-161-403-72
8	160.4	99.0	1763	11	US-09-244-805-57
9	160.4	99.0	1763	11	US-09-245-277-57
10	160.4	99.0	1763	17	US-10-792-481-57
11	160.4	99.0	4346	15	US-10-161-403-113
12	155.6	96.0	243	17	US-10-310-695-2
13	152.4	94.1	17458	15	US-10-055-001A-25
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16	152.4	94.1	17476	15	US-10-055-001A-24	Sequence 24, Appl
17	152.4	94.1	17476	15	US-10-385-546-7	Sequence 7, Appl
18	152.4	94.1	17476	15	US-10-385-546-7	Sequence 7, Appl
19	152.4	94.1	17681	15	US-10-055-001A-26	Sequence 26, Appl
20	152.4	94.1	17681	15	US-10-055-001A-26	Sequence 26, Appl
21	152.2	94.0	158	13	US-10-403-232-181	Sequence 181, App
22	150.8	93.1	4470	15	US-10-151-690-21	Sequence 21, Appl
23	150.8	93.1	4892	16	US-10-357-268-1	Sequence 1, Appl
24	150.8	93.1	5584	15	US-10-151-690-61	Sequence 61, Appl
25	150.8	93.1	17862	15	US-10-055-001A-23	Sequence 23, Appl
26	150.8	93.1	17862	15	US-10-055-001A-23	Sequence 23, Appl
27	150.8	93.1	18691	15	US-10-055-001A-13	Sequence 13, Appl
28	150.8	93.1	18691	15	US-10-055-001A-13	Sequence 13, Appl
29	150.6	93.0	233	13	US-10-301-849A-16	Sequence 16, Appl
30	150.6	93.0	233	13	US-10-403-232-177	Sequence 177, App
31	149.2	92.1	4428	15	US-10-151-690-62	Sequence 62, Appl
32	149.2	92.1	4470	15	US-10-151-690-21	Sequence 21, Appl
33	149.2	92.1	4627	15	US-10-151-690-63	Sequence 63, Appl
34	149.2	92.1	4627	15	US-10-151-690-64	Sequence 64, Appl
35	149.2	92.1	4892	16	US-10-357-268-1	Sequence 1, Appl
36	149.2	92.1	5584	15	US-10-151-690-61	Sequence 61, Appl
37	149	92.0	233	13	US-10-403-232-179	Sequence 179, App
38	148.4	91.6	2959	13	US-10-270-176-8	Sequence 8, Appl
39	148.4	91.6	3663	13	US-10-270-176-3	Sequence 3, Appl
40	148.4	91.6	3695	13	US-10-270-176-13	Sequence 13, Appl
41	148.4	91.6	4782	13	US-10-270-176-20	Sequence 20, Appl
42	148.4	91.6	5646	13	US-10-270-176-41	Sequence 41, Appl
43	148.4	91.6	5706	13	US-10-270-176-40	Sequence 40, Appl
44	148.4	91.6	5739	13	US-10-270-176-9	Sequence 9, Appl
45	148.4	91.6	5771	13	US-10-270-176-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
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; Sequence 16, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-310-695-16

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Qy	61	TTTTACAGTATTATGATGTCGTTTTTTATGCAAAATCTAATTAATATATGATATTA	120	
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Qy	121	TATCATTTTACGTTCTCGTTTCAGCTTTTTTATATACTA	162	
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RESULT 2				

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US-10-403-232-175
; Sequence 175, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiuqeng
; APPLICANT: de Ramond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 175
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-175

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Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162
Db 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

RESULT 3
US-10-627-711-10
; Sequence 10, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 168
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-10

Query Match          100.0%; Score 162; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTG 60
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QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

US-10-403-232-173
; Sequence 173, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiuqeng
; APPLICANT: de Ramond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-173

Query Match          99.0%; Score 160.4; DB 13; Length 243;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTG 60
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTG 60
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162
Db 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

RESULT 5
US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: ENENKEL, BARBARA
; APPLICANT: DROGE, PETER
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DESE:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

Query Match          99.0%; Score 160.4; DB 17; Length 243;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTG 60
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAAGTGCATATGTTG 60
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
```

```
QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162

RESULT 6
US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 99.0%; Score 160.4; DB 17; Length 248;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 60
Db 6 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 65

QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 120
Db 66 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 125

QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 126 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 167

RESULT 7
US-10-161-403-72
; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: attp
US-10-161-403-72

Query Match 99.0%; Score 160.4; DB 15; Length 282;
Best Local Similarity 99.4%; Pred. No. 3.5e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 60
Db 15 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 74

QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 120
Db 75 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 134

QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 135 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 176

RESULT 8
US-09-244-805-57/c
; Sequence 57, Application US/09244805
; Publication No. US20030203840A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukowski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/074,518
; EARLIER FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,135
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57

Query Match 99.0%; Score 160.4; DB 11; Length 1763;
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 60
Db 431 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATCATAGTAGTGCATGATGTTGTG 372

QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 120
Db 371 TTTTACAGTATTAGTAGTCTGTTTTATGCGAAATCTAATTAATATATGATATTTA 312

QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 311 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 270

RESULT 9
```

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US-09-245-277-57/c
; Sequence 57, Application US/09245277
; Publication No. US20030211984A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: JHU1530-3
; CURRENT APPLICATION NUMBER: US/09/245,277
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; NAME/KEY: misc.feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57

Query Match          99.0%; Score 160.4; DB 11; Length 1763;
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 60
Db 431 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 372
QY 61 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
Db 371 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 312
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
Db 311 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 270

RESULT 10
US-10-792-481-57/c
; Sequence 57, Application US/10792481
; Publication No. US20040152658A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimsch, Holger
; APPLICANT: Kumer, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/10/792,481
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/244,805
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763

Query Match          99.0%; Score 160.4; DB 11; Length 1763;
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 60
Db 431 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 372
QY 61 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
Db 371 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 312
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
Db 311 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 270

RESULT 11
US-10-161-403-113
; Sequence 113, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 4346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSV40-193attpsensePur Plasmid
US-10-161-403-113

Query Match          99.0%; Score 160.4; DB 15; Length 4346;
Best Local Similarity 99.4%; Pred. No. 7.6e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 60
Db 4070 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTCATTGATTCATAGTCGACATGTTG 4129
QY 61 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
Db 4130 TTTTACAGTATTATGAGTCGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 4189
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
Db 4190 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 4231

```

RESULT 12
US-10-310-695-2
; Sequence 2, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:0190S
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-310-695-2

Query Match 96.0%; Score 155.6; DB 17; Length 243;
Best Local Similarity 97.5%; Pred. No. 3.6e-24;
Matches 158; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||
Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||

RESULT 13
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||
Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||

RESULT 14
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||
Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||

RESULT 15
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 94.1%; Score 152.4; DB 15; Length 17476;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 16578 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 16637

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||
Db 16638 TATCAATTTACGTTCTCGTTCAGCTTTTATGACAAACTTG 16679
|||

RESULT 14
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 60
|||
Db 13188 TCGACTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGCACTGCGATGTTGTG 13129
|||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 120
|||
Db 13128 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTATATATTGATATTTA 13069
|||

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATATCAACTTG 162
|||
Db 13068 TATCAATTTACGTTCTCGTTCAGCTTTTATGACAAACTTG 13027
|||

RESULT 15
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 94.1%; Score 152.4; DB 15; Length 17476;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCGATATCTGTG	60
Db	16536	TCGACTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCGATATCTGTG	16595
Qy	61	TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA	120
Db	16596	TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA	16655
Qy	121	TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG	162
Db	16656	TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG	16697

Search completed: September 10, 2004, 00:14:08
 Job time : 204.654 secs

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OM nucleic - nucleic search, using sw model
Run on: September 9, 2004, 15:48:15 ; Search time 1118.24 Seconds
(without alignments)
6279.120 Million cell updates/sec

Title: US-10-082-772B-4
Perfect score: 162
Sequence: 1 tctgttacaggctcaataa.....agctttttatactaacttg 162

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_btg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	162	100.0	162	6	AX092115	AX092115 Sequence
2	162	100.0	172	7	LAMPRCB	M12459 Bacterioph
3	160.4	99.0	243	6	AX092113	AX092113 Sequence
4	160.4	99.0	361	7	LAMINTATT	M23841 Bacterioph
5	160.4	99.0	610	6	AX101000	AX101000 Sequence
6	160.4	99.0	1688	9	MACHSS	D85521 Macaca fasc
7	160.4	99.0	1763	6	BD225932	BD225932 Immediate
8	160.4	99.0	2758	3	PFAHRPC	M17028 P.falciparu
9	160.4	99.0	3485	12	AF178449	AF178449 Integrati
10	160.4	99.0	3485	12	AF178450	AF178450 Integrati
11	160.4	99.0	4105	12	AF271663	AF271663 Cloning v
12	160.4	99.0	4190	12	XXU13848	U13848 pExcell clo
13	160.4	99.0	4549	12	AF178452	AF178452 Integrati
14	160.4	99.0	4549	12	AF178453	AF178453 Integrati
15	160.4	99.0	5641	6	AX113748	AX113748 Sequence
16	160.4	99.0	5670	6	AX113749	AX113749 Sequence
17	160.4	99.0	5826	6	AX113746	AX113746 Sequence
18	160.4	99.0	6000	12	U66308	U66308 Expression
19	160.4	99.0	6043	6	AR399301	AR399301 Sequence
20	160.4	99.0	6043	6	AX370644	AX370644 Sequence
21	160.4	99.0	6071	6	AX113747	AX113747 Sequence
22	160.4	99.0	7176	12	AF178451	AF178451 Integrati
23	160.4	99.0	42529	12	CVU39284	U39284 Cloning vec
24	160.4	99.0	42530	12	CVU39285	U39285 Cloning vec
25	160.4	99.0	42531	12	CVU39286	U39286 Cloning vec
26	160.4	99.0	42704	12	CVU37692	U37692 Cloning vec
27	160.4	99.0	48502	7	LAMCG	J02459 Bacterioph
28	158.8	98.0	243	6	AX092116	AX092116 Sequence
29	150.8	93.1	4204	6	BD263378	BD263378 Compositi
30	150.8	93.1	4208	6	BD263379	BD263379 Compositi
31	150.8	93.1	4470	6	BD263377	BD263377 Compositi
32	150.8	93.1	4939	6	BD263381	BD263381 Compositi
33	150.8	93.1	5584	6	BD263402	BD263402 Compositi
34	150.8	93.1	18691	12	CV311874	AJ311874 Cloning v
35	150.8	93.1	18691	12	CV311874	AJ311874 Cloning v
36	150.6	93.0	233	6	BD263225	BD263225 Compositi
37	150.6	93.0	233	6	AX787499	AX787499 Sequence
38	149.2	92.1	4165	6	BD263380	BD263380 Compositi
39	149.2	92.1	4204	6	BD263378	BD263378 Compositi
40	149.2	92.1	4208	6	BD263379	BD263379 Compositi
41	149.2	92.1	4470	6	BD263377	BD263377 Compositi
42	149.2	92.1	4939	6	BD263381	BD263381 Compositi
43	149.2	92.1	5156	6	BD263382	BD263382 Compositi
44	149.2	92.1	5584	6	BD263402	BD263402 Compositi
45	149	92.0	233	6	BD263226	BD263226 Compositi

ALIGNMENTS

RESULT 1
AX092115
LOCUS AX092115
DEFINITION Sequence 4 from Patent WO0116345.
ACCESSION AX092115
VERSION AX092115.1 GI:13444358
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
Drooge, P.
AUTHORS
TITLE Sequence-specific dna recombination in eukaryotic cells
JOURNAL Patent: WO 0116345-A 4 08-MAR-2001;
PAT 21-MAR-2001

Pred. No. is the number of results predicted by chance to have a

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    Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:562"
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  Best Local Similarity 100.0%; Pred. No. 7.2e-21;
  Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  DB 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  QY 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
  DB 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
  QY 121 TATCATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 162
  DB 121 TATCATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 162
RESULT 2
LAMPRCB
LOCUS
  DEFINITION Bacteriophage lambda site specific recombinant DNA (attr).
  ACCESSION M12459
  VERSION M12459.1 GI:215191
  KEYWORDS
  SOURCE
  ORGANISM
    Bacteriophage lambda
    Bacteriophage lambda
    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
    Lambda-like viruses.
  1 (bases 1 to 172)
  Bushman,W., Thompson,J.F., Vargas,L. and Landy,A.
  TITLE Control of directionality in lambda site specific recombination
  JOURNAL Science 230 (4728), 906-911 (1985)
  MEDLINE 86044513
  PUBMED 2932798
  COMMENT
    Original source text: Bacteriophage lambda DNA.
    Circular phage DNA (attP) and linear bacterial DNA (attB) undergo
    integrative recombinations to yield attL and attR. AttL and attR
    can undergo excisive recombination. Positions 159-165 demark the 7
    base pair overlap region.
  Location/Qualifiers
    1..172
    /organism="Bacteriophage lambda"
    /mol_type="genomic DNA"
    /db_xref="taxon:10710"
ORIGIN
  Query Match      100.0%; Score 162; DB 7; Length 172;
  Best Local Similarity 100.0%; Pred. No. 7.1e-21;
  Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  DB 11 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 70
  QY 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
  DB 71 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 130
  QY 121 TATCATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 162
  DB 131 TAICATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 172
RESULT 3
AX092113

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LOCUS
  AX092113
  DEFINITION Sequence 2 from Patent WO0116345.
  ACCESSION AX092113
  VERSION AX092113.1 GI:13444356
  KEYWORDS
  SOURCE
  ORGANISM
    Bacteriophage lambda
    Bacteriophage lambda
    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
    Lambda-like viruses.
  1
  Droege,P.
  TITLE Sequence-specific dna recombination in eukaryotic cells
  JOURNAL Patent: WO 0116345-A 2 08-MAR-2001;
  Droege, Peter (DB)
  FEATURES
    Location/Qualifiers
      1..243
      /organism="Bacteriophage lambda"
      /mol_type="unassigned DNA"
      /db_xref="taxon:10710"
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  Query Match      99.0%; Score 160.4; DB 6; Length 243;
  Best Local Similarity 99.4%; Pred. No. 1.3e-20;
  Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  DB 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  QY 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
  DB 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
  QY 121 TATCATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 162
  DB 121 TATCATTTTACGCTTCTCGTTCAGCTTTTATATACTAACTTG 162
RESULT 4
LAMINTATT/c
LOCUS
  DEFINITION Bacteriophage lambda int gene region.
  ACCESSION M23841
  VERSION M23841.1 GI:215177
  KEYWORDS site-specific recombination.
  SOURCE Bacteriophage lambda
  ORGANISM
    Bacteriophage lambda
    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
    Lambda-like viruses.
  1 (bases 1 to 361)
  Schmeissner,U., McKenney,K., Rosenberg,K. and Court,D.
  TITLE Removal of a terminator structure by RNA processing regulates int
  gene expression
  JOURNAL J. Mol. Biol. 176 (1), 39-53 (1984)
  MEDLINE 84242838
  PUBMED 6234400
  COMMENT Original source text: Bacteriophage lambda DNA.
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    Location/Qualifiers
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      /mol_type="genomic DNA"
      /db_xref="taxon:10710"
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  Best Local Similarity 99.4%; Pred. No. 1.2e-20;
  Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 60
  DB 259 TCTGTTACAGGTCACATAACATCACTAGTAGTTCGATTCATAGTGCATATGTTGG 200
  QY 61 TTTTACAGTATTATGTCGCTGTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120

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Db      199 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 140
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QY      121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
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Db      139 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 98
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RESULT 5
AX101000
LOCUS      610 bp      DNA      linear      PAT 10-APR-2001
DEFINITION      Sequence 1 from Patent WO0121780.
ACCESSION      AX101000
VERSION      AX101000.1 GI:13619857
SOURCE      Nicotiana tabacum (common tobacco)
ORGANISM      Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE      1
AUTHORS      Meyer, P.L. and Zubko, E.L.
TITLE      Targeted gene removal
JOURNAL      Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
FEATURES
source      1..610
            /organism="Nicotiana tabacum"
            /mol_type="unassigned DNA"
            /db_xref="taxon:4097"

ORIGIN
Query Match      99.0%; Score 160.4; DB 6; Length 610;
Best Local Similarity 99.4%; Pred. No. 1.1e-20;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTAGCTGCATATGTTGTG 60
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Db      139 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTAGCTGCATATGTTGTG 198
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QY      61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
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Db      199 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 258
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QY      121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
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Db      259 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 300
      |||

RESULT 6
MACHSS/c
LOCUS      1668 bp      mRNA      linear      PRI 06-FEB-1999
DEFINITION      Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
subunit, complete cds.
ACCESSION      D85521
VERSION      D85521.1 GI:1345405
KEYWORDS      Hydroxysteroid sulfotransferase subunit.
SOURCE      Macaca fascicularis (crab-eating macaque)
ORGANISM      Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE      1 (bases 1 to 1668)
AUTHORS      Ogura, K., Satsukawa, M., Kato, K., Okuda, H. and Watabe, T.
TITLE      Molecular cloning of monkey liver hydroxysteroid sulfotransferase
Unpublished
JOURNAL
REFERENCE      2 (bases 1 to 1668)
AUTHORS      Ogura, K.
TITLE      Direct Submission
JOURNAL      Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Pharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel: +81-426-76-4518,

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FEATURES
source      Location/Qualifiers
            1..1668
            /organism="Macaca fascicularis"
            /mol_type="mRNA"
            /db_xref="taxon:9541"
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            /sex="male"
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            /clone_lib="lambda gt11"
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            /db_xref="GI:1345406"
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            LPRELPFWE"

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Query Match      99.0%; Score 160.4; DB 9; Length 1668;
Best Local Similarity 99.4%; Pred. No. 8.5e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTAGCTGCATATGTTGTG 60
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Db      391 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTAGCTGCATATGTTGTG 332
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QY      61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
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Db      331 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 272
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QY      121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
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Db      271 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 230
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RESULT 7
BD225932/c
LOCUS      1763 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Immediate early gene and method for using the same.
ACCESSION      BD225932
VERSION      BD225932.1 GI:33035702
KEYWORDS      JP 2002512772-A/49.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 1763)
AUTHORS      Worley, P.F., Lanahan, A., Goetz, B., Hiemisch, H., Kuner, R.,
Scheek, S., Nikolich, K. and Zhukovski, E.
TITLE      Immediate early gene and method for using the same
JOURNAL      Patent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
BIOSCIENCE AG
COMMENT      OS Rattus norvegicus (rat)
            PN JP 2002512772-A/49
            PD 08-MAY-2002
            PF 05-FEB-1999 JP 2000530634
            PR 09-FEB-1998 US 60/074135,12-FEB-1998 US 60/074518 PI
            PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI
            ROHINI KUNER,
            PI SIGRID SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC
            C12N15/09, A61K31/711, A61K48/00, A61P25/00, A61P25/28, C07H21/04, PC
            C07K34/47,
            PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08 PC
            C12Q1/68, G01N33/53,
            PC C12N15/00, C12N5/00
            CC n is either a, t, g, or c

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JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
 Science I Building, Ames, IA 50011, USA

FEATURES
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 /lab_host="Escherichia coli"

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 1. .385
 /notes="RGKgamma"

misc_feature
 668. .915
 /note="attP; attachment site from bacteriophage lambda"

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CDS
 complement (1327. .1986)
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protein_id="AAF86671.1"
 /db_xref="GI:9294787"

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 SSLWSYHDDFRQFLHYQSDVACYGENLAYFPKFIENMFVSNPWSFTSFDLNV
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complement (2754. .3137)
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protein_id="AAF86670.1"
 /db_xref="GI:9294786"

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misc_feature
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 /note="multiple cloning site"

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 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCACTAAGTAGTTGATTCATAGTCACTGACTGCATATGTTG 60
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QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATTAATACTAAGTTG 162
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 Db 793 TATCATTTTACGTTCTCGTTACGCTTTTATTAATACTAAGTTG 834
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RESULT 10
 AF178450
 LOCUS 3485 bp DNA linear SYN 20-JUL-2000
 DEFINITION Integration vector pCD11PSK chloramphenicol transacetylase (cat)
 and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
 ACCESSION AF178450
 VERSION AF178450.1 GI:9294788
 KEYWORDS Integration vector pCD11PSK
 ORGANISM Integration vector pCD11PSK
 REFERENCE 1 (bases 1 to 3485)
 AUTHORS Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
 TITLE Genetic system for reversible integration of DNA constructs and

lacZ gene fusions into the Escherichia coli chromosome

JOURNAL Plasmid 43 (1), 12-23 (2000)
 MEDLINE 20079288
 PUBMED 10610816

REFERENCE 2 (bases 1 to 3485)
 AUTHORS Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
 Science I Building, Ames, IA 50011, USA

FEATURES
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 668. .915
 /note="attP; attachment site from bacteriophage lambda"

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CDS
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 /db_xref="GI:9294790"

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 SSLWSYHDDFRQFLHYQSDVACYGENLAYFPKFIENMFVSNPWSFTSFDLNV
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complement (2754. .3137)
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complement (2754. .3137)
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protein_id="AAF86672.1"
 /db_xref="GI:9294789"

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misc_feature
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 /note="multiple cloning site"

ORIGIN
 Query Match 99.0%; Score 160.4; DB 12; Length 3485;
 Best Local Similarity 99.4%; Pred. No. 7.2e-21;
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QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATTAATACTAAGTTG 162
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RESULT 11
 AF271663
 LOCUS 4105 bp DNA circular SYN 11-JUL-2000
 DEFINITION Cloning vector pLDR9, complete sequence.
 ACCESSION AF271663
 VERSION AF271663.1 GI:9022390
 KEYWORDS

RESULT 12
XXU13848/c
LOCUS

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/note="bacteriophage f1 origin of replication for
production of single-stranded DNA; base 2933 represents
the first base of the newly synthesized single strand"
/direction=right
3847..4094
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3932..3947
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ORIGIN
Query Match          99.0%; Score 160.4; DB 12; Length 4190;
Best Local Similarity 99.4%; Pred. No. 6.9e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCACTCAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 60
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Db 4089 TCTGTTACAGGTCACCTAATACCACTCAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 4030
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QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
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RESULT 13
AF178452
LOCUS
DEFINITION
Integration vector pCD13PKS 4549 bp DNA linear SYN 20-JUL-2000
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION
AF178452
VERSION
AF178452.1 GI:9294794
KEYWORDS
Integration vector pCD13PKS
SOURCE
Integration vector pCD13PKS
ORGANISM
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 4549)
AUTHORS
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE
Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL
Plasmid 43 (1), 12-23 (2000)
MEDLINE
20079288
PUBMED
10610816
REFERENCE
2 (bases 1 to 4549)
AUTHORS
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
FEATURES
Location/Qualifiers
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668..915
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complement(1798..2652)
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ILRSVALVPAABEELDFVPEQDLFEALNETLTLWNSPPDWAGDNRNVLTLSRIWYSA
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Best Local Similarity 99.4%; Pred. No. 6.8e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCACTCAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 60
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Db 673 TCTGTTACAGGTCACCTAATACCACTCAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 732
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QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
|||||
Db 733 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 792
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QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
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RESULT 14
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LOCUS
DEFINITION
Integration vector pCD13PKS 4549 bp DNA linear SYN 20-JUL-2000
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION
AF178453
VERSION
AF178453.1 GI:9294797
KEYWORDS
Integration vector pCD13PKS
SOURCE
Integration vector pCD13PKS
ORGANISM
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 4549)
AUTHORS
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE
Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL
Plasmid 43 (1), 12-23 (2000)
MEDLINE
20079288
PUBMED
10610816
REFERENCE
2 (bases 1 to 4549)
AUTHORS
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
FEATURES
Location/Qualifiers
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/organism="Integration vector pCD13PKS"
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/note="R6Kgamma"
668..915
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complement(1798..2652)
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EHSVALGPAABEELFDPVPEODLPEALNETLWNSPDPDWAGDERNVVLTLSRWYSA
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ORIGIN

Query Match 99.0%; Score 160.4; DB 12; Length 4549;
Best Local Similarity 99.4%; Pred. No. 6.8e-21; Mismatches 1; Indels 0; Gaps 0;
Matches 161; Conservative 0;
QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCGACTGCATATGTTGTG 60
Db TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCGACTGCATATGTTGTG 732
QY 61 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
Db TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 792
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
Db TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 834

RESULT 15
AX113748
LOCUS AX113748 5641 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 13 from Patent WO0127322.
ACCESSION AX113748
VERSION AX113748.1 GI:13939915
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Zyskind,J.
TITILE Chitobias as a reporter enzyme
JOURNAL Patent: WO 0127322-A 13 19-APR-2001;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
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ORIGIN

Query Match 99.0%; Score 160.4; DB 6; Length 5641;
Best Local Similarity 99.4%; Pred. No. 6.5e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
Db TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 4822
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 162
Db TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAACTTG 4864

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